

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:38:20 ; Search time 88.9271 Seconds
(without alignments)
1488.535 Million cell updates/sec

Title: US-10-070-532-4
Perfect score: 1937
Sequence: 1 MEPSATPGAQMGPVPPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1937	100.0	369	4	AAU00439	Aau00439 Human neu
2	1909	98.6	369	2	AAW06125	Aaw06125 Neuropept
3	1884	97.3	402	2	AAW06124	Aaw06124 Neuropept
4	1875	96.8	372	4	AAU00440	Aau00440 Human neu
5	1875	96.8	389	2	AAW80805	Aaw80805 Amino aci
6	1875	96.8	389	4	AAU11187	Aau11187 Human G p
7	1875	96.8	389	5	ABB08208	Abb08208 G-protein
8	1875	96.8	425	2	AAW80456	Aaw80456 G-protein
9	1875	96.8	425	4	AAU11188	Aau11188 Human G p

10	1875	96.8	425	4	AAU11186	Aau11186	Human	G p
11	1875	96.8	425	4	AAB67079	Aab67079	Human	HFG
12	1875	96.8	425	5	AAG78345	Aag78345	Human	HFG
13	1875	96.8	425	6	ABP81941	Abp81941	Human	ore
14	1875	96.8	425	7	ABG75058	Abg75058	Human	ore
15	1875	96.8	425	7	ADK52564	Adk52564	Hematolog	
16	1875	96.8	425	8	ADL22443	Adl22443	Human	ore
17	1875	96.8	425	8	ADL22428	Adl22428	Human	ore
18	1875	96.8	425	8	ADO29106	Ado29106	Human	nov
19	1872	96.6	377	2	AAW06126	Aaw06126	Neuropept	
20	1870	96.5	425	4	ABB56378	Abb56378	Non-endog	
21	1869	96.5	425	4	AAU00438	Aau00438	Human	neu
22	1869	96.5	425	4	AAB67489	Aab67489	Amino aci	
23	1858.5	95.9	401	5	AAG78346	Aag78346	Human	HFG
24	1842	95.1	425	4	AAE04740	Aae04740	Cynomolgo	
25	1782	92.0	364	4	AAU00442	Aau00442	Human	neu
26	1757	90.7	416	8	ADO29107	Ado29107	Mouse	nov
27	1755	90.6	427	4	AAB47300	Aab47300	Dog	orexi
28	1326.5	68.5	460	4	AAB61970	Aab61970	Rat	HCRTR
29	1326.5	68.5	460	6	ABG73515	Abg73515	Rat	OX2R
30	1319.5	68.1	444	4	AAB61968	Aab61968	Canine	wi
31	1316.5	68.0	444	4	AAB84416	Aab84416	Amino aci	
32	1315.5	67.9	443	8	ADO29110	Ado29110	Mouse	nov
33	1313.5	67.8	444	4	AAB98007	Aab98007	Human	hyp
34	1313.5	67.8	444	4	AAB61969	Aab61969	Human	HCR
35	1313.5	67.8	444	6	ABG73514	Abg73514	Human	OX2
36	1313.5	67.8	444	6	ABP81942	Abp81942	Human	ore
37	1313.5	67.8	444	7	ABG75059	Abg75059	Human	ore
38	1313.5	67.8	444	8	ADO29109	Ado29109	Human	nov
39	1312.5	67.8	444	2	AAU03649	Aay03649	Human	7-t
40	1308.5	67.6	444	4	ABB56379	Abb56379	Non-endog	
41	1279	66.0	263	2	AAR91233	Aar91233	Rabbit	G-
42	1279	66.0	263	2	AAW11236	Aaw11236	G-protein	
43	1133.5	58.5	330	4	AAB61971	Aab61971	Canine	na
44	966	49.9	327	4	AAB61972	Aab61972	Canine	na
45	499.5	25.8	430	8	ADJ87508	Adj87508	Murine	re

ALIGNMENTS

RESULT 1

AAU00439

ID AAU00439 standard; protein; 369 AA.

XX

AC AAU00439;

XX

DT 17-MAY-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 1.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;

KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;

KW cardiovascular disorder; autoimmune disorder; infectious disorder;

KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;

KW protein co-ordinate data.

XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 47. .72
FT /label= TM1
FT /note= "Transmembrane region 1"
FT Region 83. .106
FT /label= TM2
FT /note= "Transmembrane region 2"
FT Region 112. .142
FT /label= TM3
FT /note= "Transmembrane region 3"
FT Region 163. .189
FT /label= TM4
FT /note= "Transmembrane region 4"
FT Region 214. .239
FT /label= TM5
FT /note= "Transmembrane region 5"
FT Region 299. .327
FT /label= TM6
FT /note= "Transmembrane region 6"
FT Region 335. .363
FT /label= TM7
FT /note= "Transmembrane region 7"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR N-PSDB; AAS00492.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 3; Fig 5; 385pp; English.
XX
CC The present sequence represents human neuropeptide receptor splice
CC variant 1. Two splice variants (AAU00439-AAU00440) and a possible mutant
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
CC described. The neuropeptide receptor shows sequence homology to the
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
CC neuropeptide receptor are useful for diagnosing, preventing, or treating
CC a pathological condition in a subject related to the central nervous and
CC peripheral nervous systems (CNS and PNS). The polypeptides and
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart

CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
CC diabetes mellitus. In particular they are useful for preventing, treating
CC or ameliorating a medical condition in a mammal such as obesity/eating
CC behaviour disorders, narcolepsy, neurological disease, addiction to
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
CC headaches and anxiety disorders. The polynucleotides encoding the
CC neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases

XX

SQ Sequence 369 AA;

Query Match 100.0%; Score 1937; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.9e-189;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSLGIWAVSLAIMVPQA 180
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Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGLPWSLL 369
      |||
Db    361 LSGLPWSLL 369
```

RESULT 2

AAW06125

ID AAW06125 standard; protein; 369 AA.

XX

AC AAW06125;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 47. .72

FT /note= "Transmembrane region-1"

FT Domain 83. .106

FT /note= "Transmembrane region-2"

FT Domain 112. .142

FT /note= "Transmembrane region-3"

FT Domain 163. .189

FT /note= "Transmembrane region-4"

FT Domain 214. .239

FT /note= "Transmembrane region-5"

FT Domain 299. .327

FT /note= "Transmembrane region-6"

FT Domain 335. .363

FT /note= "Transmembrane region-7"

XX

PN WO9634877-A1.

XX

PD 07-NOV-1996.

XX

PF 05-MAY-1995; 95WO-US005616.

XX

PR 05-MAY-1995; 95WO-US005616.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Soppet DR, Li Y, Rosen CA;

XX

DR WPI; 1996-506094/50.

DR N-PSDB; AAT42827.

XX

PT Human neuro-peptide receptor polypeptide(s) - used to identify

PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of

PT obesity, Alzheimer's disease, epilepsy, etc.

XX

PS Disclosure; Page 51-52; 77pp; English.

XX

CC The sequence represents human adult hypothalamus neuropeptide receptor
CC splice variant-1, which retains activity corresponding to the mature
CC receptor (AAW06124), which is structurally related to the G-protein-
CC coupled receptor family. The receptor variant contains 7 transmembrane
CC regions. The receptor may be produced in recombinant form and used in a
CC drug screening assay for isolation of receptor-agonists and -antagonists,
CC which may be used as anorectic, antitumour, anticholesterolemic,
CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
CC The receptor itself and its corresponding antibody may also be used in
CC therapy and diagnosis

XX

SQ Sequence 369 AA;

Query Match 98.6%; Score 1909; DB 2; Length 369;

Best Local Similarity 98.6%; Pred. No. 1.4e-186;

Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGLPWSLL 369
      |||
Db    361 LSGLPWSLL 369

```

RESULT 3

AAW06124

ID AAW06124 standard; protein; 402 AA.

XX

AC AAW06124;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor.

XX

KW Human; neuropeptide receptor; drug screening; receptor-agonist;
KW receptor-antagonist; anorectic; antitumour; anticholesterolemic;
KW neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;
KW gene therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Domain 47. .72

FT /note= "Transmembrane region-1"

FT Domain 83. .106

FT /note= "Transmembrane region-2"

FT Domain 112. .142

FT /note= "Transmembrane region-3"

FT Domain 163. .189

FT /note= "Transmembrane region-4"

FT Domain 214. .239
 FT /note= "Transmembrane region-5"
 FT Domain 299. .327
 FT /note= "Transmembrane region-6"
 FT Domain 335. .363
 FT /note= "Transmembrane region-7"
 XX
 PN WO9634877-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 05-MAY-1995; 95WO-US005616.
 XX
 PR 05-MAY-1995; 95WO-US005616.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 1996-506094/50.
 DR N-PSDB; AAT42826.
 XX
 PT Human neuro-peptide receptor polypeptide(s) - used to identify
 PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
 PT obesity, Alzheimer's disease, epilepsy, etc.
 XX
 PS Claim 1; Page 49-50; 77pp; English.
 XX
 CC The sequence represents a human adult hypothalamus neuropeptide receptor,
 CC structurally related to the G-protein-coupled receptor family. Splice
 CC variants are given in AAW06125-26. The receptor contains 7 transmembrane
 CC regions. The receptor may be produced in recombinant form and used in a
 CC drug screening assay for isolation of receptor-agonists and -antagonists,
 CC which may be used as anorectic, antitumour, anticholesterolemic,
 CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
 CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
 CC The receptor itself and its corresponding antibody may also be used in
 CC therapy and diagnosis
 XX
 SQ Sequence 402 AA;

Query Match 97.3%; Score 1884; DB 2; Length 402;
 Best Local Similarity 98.9%; Pred. No. 5.7e-184;
 Matches 359; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db	1	MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180

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QY      181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db      181 AVMECSSVLPPELANRTRLFSVCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

QY      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
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Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

QY      301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

QY      361 LSG 363
      |||
Db      361 LSG 363

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RESULT 4

AAU00440

ID AAU00440 standard; protein; 372 AA.

XX

AC AAU00440;

XX

DT 18-JUN-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 2.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;

KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;

KW cardiovascular disorder; autoimmune disorder; infectious disorder;

KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;

KW protein co-ordinate data.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Region	47. .72
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FT		/label= TM1
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FT		/note= "Transmembrane region 1"
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FT	Region	83. .106
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FT		/label= TM2
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FT		/note= "Transmembrane region 2"
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FT	Region	112. .142
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FT		/label= TM3
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FT		/note= "Transmembrane region 3"
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FT	Region	163. .189
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FT		/label= TM4
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FT		/note= "Transmembrane region 4"
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FT	Region	214. .239
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FT		/label= TM5
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FT		/note= "Transmembrane region 5"
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FT	Region	299. .327
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FT		/label= TM6
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FT		/note= "Transmembrane region 6"
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FT	Region	335. .363
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FT		/label= TM7
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FT /note= "Transmembrane region 7"
 XX
 PN WO200117532-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024518.
 XX
 PR 10-SEP-1999; 99US-00393696.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 2001-183276/18.
 DR N-PSDB; AAS00493.
 XX
 PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
 PT useful for preventing, treating or ameliorating obesity, narcolepsy,
 PT neurological disease and addiction to narcotics, nicotine and alcohol.
 XX
 PS Claim 3; Fig 6; 385pp; English.
 XX
 CC The present sequence represents human neuropeptide receptor splice
 CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant
 CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
 CC described. The neuropeptide receptor shows sequence homology to the
 CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
 CC neuropeptide receptor are useful for diagnosing, preventing, or treating
 CC a pathological condition in a subject related to the central nervous and
 CC peripheral nervous systems (CNS and PNS). The polypeptides and
 CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
 CC autoimmune, nervous system or infectious disorders e.g. cancer, heart
 CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
 CC diabetes mellitus. In particular they are useful for preventing, treating
 CC or ameliorating a medical condition in a mammal such as obesity/eating
 CC behaviour disorders, narcolepsy, neurological disease, addiction to
 CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
 CC headaches and anxiety disorders. The polynucleotides encoding the
 CC neuropeptide receptor can also be used in gene therapy methods for
 CC treating such diseases
 XX
 SQ Sequence 372 AA;

Query Match 96.8%; Score 1875; DB 4; Length 372;
 Best Local Similarity 98.6%; Pred. No. 4.3e-183;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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 Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120
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 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120
 Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEKSTARRARGSSILGIWAVSLAIMVPQA 180

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Db      121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
Qy      181 AVMQSSSVLP ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db      181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy      241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db      241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
      |||
Db      361 LSG 363

```

RESULT 5

AAW80805

ID AAW80805 standard; protein; 389 AA.

XX

AC AAW80805;

XX

DT 29-JAN-1999 (first entry)

XX

DE Amino acid sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;

KW antagonist; activation; inhibition; gene therapy; antibody;

KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;

KW asthma; Parkinson's disease; acute heart failure; hypotension;

KW hypertension; urinary retention; osteoporosis; angina pectoris;

KW myocardial infarction; ulcer; allergies; psychotic disorder;

KW neurological disorder; gene mapping.

XX

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

PR 30-APR-1997; 97US-00846705.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis C;

XX

DR WPI; 1998-570286/49.

DR N-PSDB; AAV68511.

XX

PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -

PT useful as diagnostic reagents and for prevention and treatment of HIV

PT infections, cancer, osteoporosis and Parkinson's disease.

XX

PS Claim 1; Page 7; 22pp; English.

XX

CC This is the amino acid sequence of the G-protein coupled receptor,
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases by
CC detecting mutations in the HFGAN72Y gene using probes containing the
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC HFGAN72Y activity, in addition to direct administration of antisense
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC administered directly or as a vaccine to inoculate against diseases.
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene
CC to a chromosome, allowing gene inheritance to be studied through linkage
CC analysis

XX

SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 2; Length 389;
Best Local Similarity 98.6%; Pred. No. 4.5e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGPVPPGSREPSVPVPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGPVPPGSREPSVPVPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 6

AAU11187

ID AAU11187 standard; protein; 389 AA.

XX

AC AAU11187;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72Y.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72Y; bacterial infection;

KW fungal infection; protozoan infection; viral infection;

KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;

KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;

KW angina pectoris; renal disease; depression; schizophrenia; anorexia;

KW obesity; Kallman's syndrome; hypothalamic disorder;

KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;

KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need

PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.

PT infections such as bacterial, fungal, protozoan and viral infections and

PT cancers.

XX

PS Claim 8; Fig 3; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or

CC its variant, encoded by the 8 exon sequences given in the specification.

CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the

CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
 CC administered by providing to the patient DNA encoding HFGAN72 and
 CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
 CC useful for applications in the detection and treatment of disease, e.g.
 CC infections such as bacterial, fungal, protozoan and viral infections,
 CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
 CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
 CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
 CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
 CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
 CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
 CC Huntington's disease and many other diseases and disorders given in the
 CC specification. The present sequence is the human HFGAN72Y receptor being
 CC the product of a splice variant of HFGAN72

XX

SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 4; Length 389;
 Best Local Similarity 98.6%; Pred. No. 4.5e-183;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPELANRTRLFSLCHEWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRLFSVCDEWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 7

ABB08208

ID ABB08208 standard; protein; 389 AA.

XX

AC ABB08208;

XX

DT 12-MAR-2002 (first entry)

XX
 DE G-protein coupled receptor (HFGAN72Y).
 XX
 KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
 KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
 KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
 KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
 KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
 KW schizophrenia; manic depression; dementia; mental retardation;
 KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2.
 XX
 OS Homo sapiens.
 XX
 PN EP1156110-A2.
 XX
 PD 21-NOV-2001.
 XX
 PF 27-OCT-1997; 2001EP-00203010.
 XX
 PR 30-APR-1997; 97US-00846705.
 PR 27-OCT-1997; 97EP-00308554.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 XX
 PI Bergsma DJ, Ellis CE;
 XX
 DR WPI; 2002-084320/12.
 DR N-PSDB; ABA96019.
 XX
 PT New polynucleotide encoding a G-protein coupled receptor designated
 PT HFGAN72Y is useful to diagnose and treat associated diseases including
 PT cancer, infection, cardiac disease and psychotic and neurological
 PT disorders.
 XX
 PS Claim 10; Page 7; 22pp; English.
 XX
 CC The sequence represents G-protein coupled receptor HFGAN72Y. The
 CC invention relates to a novel isolated polynucleotide encoding HFGAN72Y
 CC polypeptide. The polypeptide of the invention has cytostatic, cardiant,
 CC analgesic, tranquillising, nootropic, neuroprotective, and anti-asthmatic
 CC activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
 CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
 CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
 CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
 CC expression is used to treat a subject in need of decreased HFGAN72Y
 CC activity or expression. HFGAN72Y-associated diseases include infections,
 CC particularly by HIV-1 or HIV-2, cancers, anorexia, bulimia, Parkinson's
 CC disease, cardiac diseases, ulcers, urinary retention, asthma, allergies,
 CC benign prostatic hypertrophy, and psychotic and neurological disorders
 CC including anxiety, schizophrenia, manic depression, delirium, dementia,
 CC severe mental retardation and dyskinesias such as Huntington's disease
 CC and Tourette's syndrome, and pain
 XX
 SQ Sequence 389 AA;

Query Match 96.8%; Score 1875; DB 5; Length 389;
 Best Local Similarity 98.6%; Pred. No. 4.5e-183;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFEGHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||: |||
Db    181 AVMECSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 8

AAW80456

ID AAW80456 standard; protein; 425 AA.

XX

AC AAW80456;

XX

DT 26-JAN-1999 (first entry)

XX

DE G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder.

XX

OS Homo sapiens.

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX
 PI Bergsma DJ, Ellis CE;
 XX
 DR WPI; 1998-559432/48.
 DR N-PSDB; AAV63468.
 XX
 PT New human G-protein coupled receptor HFGAN72X polypeptide and
 PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
 PT infection, cancer and Parkinson's disease.
 XX
 PS Claim 1; Page 7-8; 24pp; English.
 XX
 CC The present sequence represents a G-protein coupled receptor (HFGAN72X)
 CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
 CC diagnosing diseases related to over or under expression of HFGAN72X
 CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
 CC probes, or determining HFGAN72X protein or mRNA expression levels.
 CC HFGAN72X polypeptides are also useful for screening for compounds which
 CC affect activity of the protein. Diseases that can be treated with
 CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
 CC asthma, Parkinson's disease, acute heart failure, hypotension,
 CC hypertension, urinary retention, osteoporosis, angina pectoris,
 CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
 CC and psychotic and neurological disorders
 XX
 SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 2; Length 425;
 Best Local Similarity 98.6%; Pred. No. 5.1e-183;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGPVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGPVPPGSRPEPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA	180
Qy	181	AVMQSSSVLPCLANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363

RESULT 9

AAU11188

ID AAU11188 standard; protein; 425 AA.

XX

AC AAU11188;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X variant.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;

KW fungal infection; protozoan infection; viral infection;

KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;

KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;

KW angina pectoris; renal disease; depression; schizophrenia; anorexia;

KW obesity; Kallman's syndrome; hypothalamic disorder;

KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;

KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

DR N-PSDB; AAS17464.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.

XX

PS Claim 23; Fig 6; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and

CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
 CC useful for applications in the detection and treatment of disease, e.g.
 CC infections such as bacterial, fungal, protozoan and viral infections,
 CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
 CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
 CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
 CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
 CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
 CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
 CC Huntington's disease and many other diseases and disorders given in the
 CC specification. The present sequence is the human HFGAN72X variant,
 CC encoded by an alternative allele of HFGAN72

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;
 Best Local Similarity 98.6%; Pred. No. 5.1e-183;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGMVPPGSREPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGMVPPGSREPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPCLANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 10

AAU11186

ID AAU11186 standard; protein; 425 AA.

XX

AC AAU11186;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X.

XX
 KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;
 KW fungal infection; protozoan infection; viral infection;
 KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
 KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
 KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
 KW obesity; Kallman's syndrome; hypothalamic disorder;
 KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
 KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2001025031-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 06-APR-2001; 2001US-00828538.
 XX
 PR 08-JUN-1998; 98US-0088524P.
 PR 22-JUL-1998; 98US-0093726P.
 PR 08-JUN-1999; 99US-00328014.
 XX
 PA (ELLI/) ELLIS C E.
 PA (KWOK/) KWOK C.
 PA (BODS/) BODSWORTH N J.
 PA (HALS/) HALSEY W.
 PA (HORN/) HORN S V.
 XX
 PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;
 XX
 DR WPI; 2001-624968/72.
 XX
 PT Isolated HFGAN72 receptor useful for treatment of a patient having need
 PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
 PT infections such as bacterial, fungal, protozoan and viral infections and
 PT cancers.
 XX
 PS Claim 8; Fig 2; 75pp; English.
 XX
 CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
 CC its variant, encoded by the 8 exon sequences given in the specification.
 CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
 CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
 CC administered by providing to the patient DNA encoding HFGAN72 and
 CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
 CC useful for applications in the detection and treatment of disease, e.g.
 CC infections such as bacterial, fungal, protozoan and viral infections,
 CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
 CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
 CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
 CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
 CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
 CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
 CC Huntington's disease and many other diseases and disorders given in the
 CC specification. The present sequence is the human HFGAN72X receptor being
 CC the product of a splice variant of HFGAN72
 XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;
Best Local Similarity 98.6%; Pred. No. 5.1e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||: |||
Db    181 AVMECSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
          |||
Db    361 LSG 363
```

RESULT 11

AAB67079

ID AAB67079 standard; protein; 425 AA.

XX

AC AAB67079;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor SEQ ID NO: 13.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72; ~~receptor~~

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

XX
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR WPI; 2001-071483/08.

XX
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.

XX
PS Claim 8; Fig 7; 101pp; English.

XX
CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions

XX
SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 4; Length 425;
Best Local Similarity 98.6%; Pred. No. 5.1e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSRPEPVPDPYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
|||||
Db 1 MEPSATPGAQMGVPPGSRPEPVPDPYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCK 120
|||||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
|||||
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||: |||||
Db 181 AVMECSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||||
Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWL VYANSAANPIIYNF 360
|||||
Db 301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWL VYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 12

AAG78345

ID AAG78345 standard; protein; 425 AA.

XX

AC AAG78345;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor.

XX

OS Homo sapiens.

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR N-PSDB; AAI64172.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.

XX

PS Claim 11; Page 7-8; 24pp; English.

XX

CC The present sequence is that of a human HFGAN72X polypeptide encoded by a
CC cDNA shown in AAI64172. The specification describes a newly isolated
CC polynucleotide encoding a HFGAN72X G coupled receptor polypeptide. The
CC protein of the invention has antibacterial, fungicide, virucide,
CC protozoacide, anti-HIV, cardiant, analgesic, cytostatic, nootropic,
CC antiparkinsonian, antiulcer, antiasthmatic, tranquiliser, neuroleptic,
CC antidepressant, anticonvulsant and osteopathic activities. HFGAN72X
CC polynucleotides (PNs) are used to express HFGAN72X in vivo, to treat
CC diseases requiring increased activity or expression of HFGAN72X; for
CC recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as

CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and
CC dyskinesias

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 5; Length 425;
Best Local Similarity 98.6%; Pred. No. 5.1e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||
Db    181 AVMECSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTTALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTTALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
      |||
Db    361 LSG 363
```

RESULT 13

ABP81941

ID ABP81941 standard; protein; 425 AA.

XX

AC ABP81941;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 protein SEQ ID NO:368.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW G protein-coupled receptor modulator; antibody; immune-related disease;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer;

KW immunological-related cell proliferative disease; autoimmune disease;

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42789.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors

PT (GPCR), useful for diagnosing and designing drugs for treating conditions

PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or

PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)

CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino

CC acids. Also described: (1) an assay for the detection of a particular G

CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;

CC and (2) an isolated antibody having high specificity and high affinity or

CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in

CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an

CC antibody against a particular GPCR, and in the production of specific

CC antibodies. The peptides and antibodies are also useful for detecting the

CC presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for

CC treating immune-related diseases, growth-related diseases, cell

CC regeneration-related disease, immunological-related cell proliferative

CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,

CC atherosclerosis, bacterial, fungal, protozoan or viral infections,

CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host

CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,

CC anxiety, depression, schizophrenia, dementia, mental retardation, memory

CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX

SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 6; Length 425;
Best Local Similarity 98.6%; Pred. No. 5.1e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
|||||
Db 1 MEPSATPGAQMGVPPGSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
|||||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSI LGIWA VSLAIMVPQA 180
|||||
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy 181 AVMQSSSVLP ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||: |||||
Db 181 AVMECSSSVLP ELANRTRLF SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||||
Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVLVLV FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||||
Db 301 MVLVLV FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 14

ABG75058

ID ABG75058 standard; protein; 425 AA.

XX

AC ABG75058;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human orexin receptor 1 protein.

XX

KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;

KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;

KW cardiant; osteopathic; antilipemic.

XX

OS Homo sapiens.

XX
 PN WO2003075945-A2.
 XX
 PD 18-SEP-2003.
 XX
 PF 14-MAR-2003; 2003WO-EP002714.
 XX
 PR 14-MAR-2002; 2002EP-00005882.
 PR 15-MAR-2002; 2002EP-00006012.
 PR 20-MAR-2002; 2002EP-00006271.
 PR 25-MAR-2002; 2002EP-00006810.
 XX
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 XX
 PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
 XX
 DR WPI; 2003-748334/70.
 DR N-PSDB; ACH00818.
 XX
 PT New pharmaceutical composition comprising a nucleic acid molecule
 PT encoding proteins regulating the energy homeostasis and metabolism of
 PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
 PT obesity.
 XX
 PS Claim 3; Fig 7G; 140pp; English.
 XX
 CC The present invention relates to pharmaceutical compositions comprising
 CC the coding sequences shown in ACH00815-ACH00827, or their encoded
 CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
 CC involved in the metabolism of triglycerides and in energy homeostasis,
 CC and their coding sequences. The composition is useful for the manufacture
 CC of an agent for detecting, verifying, treating, alleviating or preventing
 CC disorders, including metabolic diseases such as obesity and other body-
 CC weight regulation disorders as well as related disorders such as
 CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
 CC hypertension, coronary heart disease, hypercholesterolaemia,
 CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
 CC organs or subjects. The coding sequences can be used in the production of
 CC transgenic animals which under- or over-produce the gene of interest. The
 CC present sequence is a protein of the invention
 XX
 SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 7; Length 425;
 Best Local Similarity 98.6%; Pred. No. 5.1e-183;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

 Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEKSTARRARGSIWVAVSLAIMVPOA 180
 |||||||||||||||| ||||||||||||||||||||||||||||||||||||

Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
 Qy 181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||: |||||:| |||||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 15

ADK52564

ID ADK52564 standard; protein; 425 AA.

XX

AC ADK52564;

XX

DT 06-MAY-2004 (first entry)

XX

DE Hematological disorder associated Gene ID 14393 encoded protein.

XX

KW cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;

KW cytostatic; thrombolytic; antiparasitic; gene therapy;

KW hematologic disorder; cancer; Sickle Cell Anemia;

KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;

KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;

KW transfusion reaction; Erythroblastosis; mechanical trauma;

KW micro-angiopathic hemolytic anemia; parasite infection.

XX

OS Homo sapiens.

XX

PN WO2003065871-A2.

XX

PD 14-AUG-2003.

XX

PF 28-JAN-2003; 2003WO-US002484.

XX

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375626P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394128P.

PR 31-JUL-2002; 2002US-0399783P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Carroll JM, Healy A, Weich NS, Kelly LM;
XX
DR WPI; 2003-731464/69.
DR N-PSDB; ADK52563.
XX
PT Identifying a compound capable of treating a hematologic disorder (e.g.
PT anemia or leukemia) comprises assaying the ability of the compound to
PT modulate the expression or activity of e.g. 131,148, 199 or 12303
PT polypeptide or nucleic acid.
XX
PS Disclosure; SEQ ID NO 22; 232pp; English.
XX
CC The invention relates to a method of identifying a compound capable of
CC treating a hematologic disorder comprises assaying the ability of the
CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
CC acid expression or polypeptide activity, thus, identifying a compound
CC capable of treating a hematologic disorder. The methods are useful in
CC diagnosing, preventing and treating hematological disorders, such as
CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
CC Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
CC associated with an increased risk of Thrombosis, Herpes, Thalassemia,
CC antibody-mediated disorders such as transfusion reactions and
CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
CC angiopathic hemolytic anemias, infections by parasites or chemical
CC injuries. The methods may also be used for identifying compounds that
CC modulate hematological disorders. This sequence corresponds to the
CC protein encoded by one of the genes modulated by the compounds.
XX
SQ Sequence 425 AA;

Query Match 96.8%; Score 1875; DB 7; Length 425;
Best Local Similarity 98.6%; Pred. No. 5.1e-183;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLEVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180

Qy    181 AVMQSSSVLP ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||
Db    181 AVMECSSSVLP ELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDL EQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
1089.110 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
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1	1909	98.6	369	4	US-08-462-509B-4	Sequence 4, Appli	
2	1909	98.6	369	5	PCT-US95-05616-4	Sequence 4, Appli	
3	1875	96.8	377	5	PCT-US95-05616-6	Sequence 6, Appli	
4	1875	96.8	389	2	US-08-846-705-2	Sequence 2, Appli	
5	1875	96.8	389	4	US-09-211-823C-23	Sequence 23, Appl	
6	1875	96.8	402	4	US-08-462-509B-2	Sequence 2, Appli	
7	1875	96.8	402	5	PCT-US95-05616-2	Sequence 2, Appli	
8	1875	96.8	425	3	US-08-846-704-2	Sequence 2, Appli	
9	1875	96.8	425	4	US-09-211-823C-22	Sequence 22, Appl	
10	1872	96.6	372	4	US-08-462-509B-6	Sequence 6, Appli	
11	1869	96.5	402	3	US-08-846-704-4	Sequence 4, Appli	

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14	1312.5	67.8	444	3	US-09-119-788-2	Sequence 2, Appli
15	1279	66.0	263	3	US-08-513-974B-54	Sequence 54, Appl
16	1279	66.0	263	3	US-08-513-974B-376	Sequence 376, App
17	1279	66.0	263	4	US-09-461-436B-54	Sequence 54, Appl
18	483.5	25.0	430	3	US-09-255-368-8	Sequence 8, Appli
19	483.5	25.0	430	4	US-09-405-558-8	Sequence 8, Appli
20	480.5	24.8	432	3	US-09-255-368-2	Sequence 2, Appli
21	480.5	24.8	432	4	US-09-405-558-2	Sequence 2, Appli
22	473.5	24.4	420	3	US-09-255-368-6	Sequence 6, Appli
23	473.5	24.4	420	4	US-09-405-558-6	Sequence 6, Appli
24	467.5	24.1	417	4	US-09-405-558-44	Sequence 44, Appl
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27	415	21.4	370	4	US-09-799-955-2	Sequence 2, Appli
28	415	21.4	370	4	US-09-799-955-3	Sequence 3, Appli
29	411.5	21.2	370	3	US-09-172-353-7	Sequence 7, Appli
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31	411	21.2	370	3	US-08-513-974B-26	Sequence 26, Appl
32	411	21.2	370	3	US-08-513-974B-323	Sequence 323, App
33	411	21.2	370	3	US-09-172-353-5	Sequence 5, Appli
34	411	21.2	370	3	US-08-776-971-21	Sequence 21, Appl
35	411	21.2	370	3	US-08-776-971-104	Sequence 104, App
36	411	21.2	370	4	US-09-799-955-5	Sequence 5, Appli
37	411	21.2	370	4	US-09-461-436B-26	Sequence 26, Appl
38	411	21.2	370	4	US-09-576-290-21	Sequence 21, Appl
39	411	21.2	370	4	US-09-576-290-104	Sequence 104, App
40	404.5	20.9	370	3	US-08-776-971-140	Sequence 140, App
41	404.5	20.9	370	4	US-09-576-290-140	Sequence 140, App
42	401.5	20.7	369	4	US-09-170-496D-178	Sequence 178, App
43	400.5	20.7	369	3	US-09-172-353-6	Sequence 6, Appli
44	400.5	20.7	369	4	US-09-799-955-6	Sequence 6, Appli
45	400.5	20.7	369	4	US-09-170-496D-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-08-462-509B-4

; Sequence 4, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/462,509B
;   FILING DATE:  05-JUN-1995
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  WO PCT/US95/05616
;   FILING DATE:  05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Wales, Michele M.
;   REGISTRATION NUMBER:  43,975
;   REFERENCE/DOCKET NUMBER:  PF168P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  301-309-8504
;   TELEFAX:  301-309-8439
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 369 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-462-509B-4

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Query Match          98.6%;  Score 1909;  DB 4;  Length 369;
Best Local Similarity 98.6%;  Pred. No. 2.6e-188;
Matches 364;  Conservative 2;  Mismatches 3;  Indels 0;  Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMQSSSVLP ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||
Db    181 AVMECSSSVLP ELANRTRLF SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGLPWSLL 369
      |||
Db    361 LSGLPWSLL 369

```


RESULT 2
 PCT-US95-05616-4
 ; Sequence 4, Application PC/TUS9505616
 ; GENERAL INFORMATION:
 ; APPLICANT: LI, ET AL.
 ; TITLE OF INVENTION: Human Neuropeptide Receptor
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
 ; ADDRESSEE: CECCHI, STEWART & OLSTEIN
 ; STREET: 6 BECKER FARM ROAD
 ; CITY: ROSELAND
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 INCH DISKETTE
 ; COMPUTER: IBM PS/2
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: WORD PERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/05616
 ; FILING DATE: concurrently
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FERRARO, GREGORY D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-268
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 369 BASE PAIRS
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: SINGLE
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE: cDNA
 PCT-US95-05616-4

Query Match 98.6%; Score 1909; DB 5; Length 369;
 Best Local Similarity 98.6%; Pred. No. 2.6e-188;
 Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA	60
Db	1	MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA	60
Qy	61	LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK	120
Db	61	LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLP ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240

Best Local Similarity 98.6%; Pred. No. 8.6e-185;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
        |||
Db     61 LVGN TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPOA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARG SILGIWAVSLAIMVPOA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||
Db    181 AVMECSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 4

US-08-846-705-2

; Sequence 2, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMAN, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,705

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-705-2

```

```

Query Match          96.8%; Score 1875; DB 2; Length 389;
Best Local Similarity 98.6%; Pred. No. 9e-185;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy      1 MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVQA 180

Qy    181 AVMQSSSVLPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||
Db    181 AVMECSSVLPELANRTRFLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363

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```

RESULT 5
US-09-211-823C-23
; Sequence 23, Application US/09211823C
; Patent No. 6664229

```

```
; GENERAL INFORMATION:
; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNETT, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-23
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Query Match          96.8%; Score 1875; DB 4; Length 389;
Best Local Similarity 98.6%; Pred. No. 9e-185;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRLYLWRDYLKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRLYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
      |||
Db    361 LSG 363
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RESULT 6

US-08-462-509B-2

; Sequence 2, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-462-509B-2

Query Match 96.8%; Score 1875; DB 4; Length 402;

Best Local Similarity 98.6%; Pred. No. 9.4e-185;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGMVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGMVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

```

```

Db      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPPA 180
Qy      181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||||:| |||||
Db      181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||||
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||||
Db      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
      |||
Db      361 LSG 363

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RESULT 7

PCT-US95-05616-2

; Sequence 2, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WORD PERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/05616

; FILING DATE: concurrently

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: FERRARO, GREGORY D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-268

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 AMINO ACIDS

; TYPE: AMINO ACID

; STRANDEDNESS:

; TOPOLOGY: LINEAR

; MOLECULE TYPE: PROTEIN
PCT-US95-05616-2

Query Match 96.8%; Score 1875; DB 5; Length 402;
Best Local Similarity 98.6%; Pred. No. 9.4e-185;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 8

US-08-846-704-2

; Sequence 2, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0


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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/846,704
; FILING DATE: 30-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-704-2

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Query Match          96.8%; Score 1875; DB 3; Length 425;
Best Local Similarity 98.6%; Pred. No. 1e-184;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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```

Qy      1 MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
      |||
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
      |||
Db      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy      181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db      181 AVMECSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
      |||
Db      361 LSG 363

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RESULT 9
 US-09-211-823C-22
 ; Sequence 22, Application US/09211823C
 ; Patent No. 6664229
 ; GENERAL INFORMATION:
 ; APPLICANT: HAGEN, JAMES JOSEPH
 ; APPLICANT: TERRETT, JONATHAN ALEXANDER
 ; APPLICANT: UPTON, NEIL
 ; APPLICANT: PIPER, DAVID
 ; APPLICANT: SMITH, MARTIN IAN
 ; APPLICANT: KENNETT, GUY ANTHONY
 ; APPLICANT: PATEL, SARASWATI R.
 ; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
 ; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
 ; TITLE OF INVENTION: ANTAGONISTS THEREOF
 ; FILE REFERENCE: P50745
 ; CURRENT APPLICATION NUMBER: US/09/211,823C
 ; CURRENT FILING DATE: 1998-12-15
 ; PRIOR APPLICATION NUMBER: US 60/069,459
 ; PRIOR FILING DATE: 1997-12-15
 ; PRIOR APPLICATION NUMBER: US 60/069,785
 ; PRIOR FILING DATE: 1997-12-16
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-211-823C-22

Query Match 96.8%; Score 1875; DB 4; Length 425;
 Best Local Similarity 98.6%; Pred. No. 1e-184;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFGHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360

Qy 361 LSG 363
 |||
Db 361 LSG 363

RESULT 10

US-08-462-509B-6

; Sequence 6, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

```
; NUMBER OF SEQUENCES: 12
```

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockiville

```
; STATE: MD
```

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

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;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

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; INFORMATION FOR SEQ ID NO: 6:
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; SEQUENCE CHARACTERISTICS:

; LENGTH: 372 amino acids

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;      TYPE:  amino acid
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;      TOPOLOGY:  linear
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; MOLECULE TYPE:  protein
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US-08-462-509B-6

Query Match 96.6%; Score 1872; DB 4; Length 372;

Best Local Similarity 98.3%; Pred. No. 1.7e-184;

Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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Db 1 MEPSATPGAQMGPVPPGSRDPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCK 120

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Db      61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
Db      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
Qy      181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
Db      361 LSG 363

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RESULT 11

US-08-846-704-4

; Sequence 4, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-846-704-4

Query Match 96.5%; Score 1869; DB 3; Length 402;
 Best Local Similarity 98.3%; Pred. No. 3.9e-184;
 Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSAVLTLSTFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSAVLTLSTFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||
Db    181 AVMECSSVLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
      |||
Db    361 LSG 363
  
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RESULT 12
 US-09-479-128-2
 ; Sequence 2, Application US/09479128
 ; Patent No. 6319710
 ; GENERAL INFORMATION:
 ; APPLICANT: Berglind Ran Olafsdottir
 ; APPLICANT: Jeffrey Gulcher
 ; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
 ; FILE REFERENCE: 2345.1005-001
 ; CURRENT APPLICATION NUMBER: US/09/479,128
 ; CURRENT FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 96.5%; Score 1869; DB 3; Length 425;
Best Local Similarity 98.3%; Pred. No. 4.2e-184;
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDPYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
|||||
Db 1 MEPSATPGAQMGVPPGSREPSVPPDPYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
|||||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
|||||
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||: |||||
Db 181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||||
Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||||
Db 301 MVVLLVFALCYLPISVLNVLKR VFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 13

US-09-426-290-2

; Sequence 2, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 444

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-426-290-2

Query Match 67.8%; Score 1313.5; DB 4; Length 444;
Best Local Similarity 70.0%; Pred. No. 7.8e-127;
Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

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Qy      17 SREPSVPVPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
      ::|| | ||:| |||||:|:|:|:|:|:| | : |||||:| | ||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCKVIPYLQAVSVSVAVL 135
      |||||:|:|:|:|:|:|:|:|:|:|:|:| | | :|||:| | ||:|:|:|
Db      84 HMRTVTNYFIVNLSLADVLTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIPLDRWYAICHPLLFKSTARRARGSSILGIWAVSLAIMVPQAAMQSSSVLPPELANR 195
      ||| | |||||:|:|:|:|:| | | : || | | :|| | | :| | ||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTVFPLANK 203

Qy     196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
      | ||:| ||| :|||:| | ||:|:|:| | | :|| ||||| |||||:| :
Db     204 TTLETVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWKRPDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVVLLV 306
      | || | || | | ||:|:|:|:|:|:| |
Db     264 RKWK-----PLQPVSQPRGPGQPTKSRMSAVAAEIKQIRARRKTARMLMVVLLV 312

Qy     307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
      ||:|||||:||||| || | || | ||||| ||||| ||||| |||||
Db     313 FAICYLPISILNVLKRVFGMFAHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSG 369
```

RESULT 14

US-09-119-788-2

; Sequence 2, Application US/09119788

; Patent No. 6166193

; GENERAL INFORMATION:

; APPLICANT: Yanagisawa, Masashi

; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES

; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/119,788

; FILING DATE: 21-JUL-1998

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-119-788-2

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Query Match          67.8%; Score 1312.5; DB 3; Length 444;
Best Local Similarity 70.0%; Pred. No. 9.9e-127;
Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

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Qy      17 SREPSVPDPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
      ::|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:| |
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYQLQAVSVSVAVL 135
      |||||:|:|:| |||||:|:|:| || | ||:| ||||| ||||:| |
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLQTVSVSVSVL 143

Qy     136 TLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA AVMQSSSVLP ELANR 195
      ||| | |||||:|:|:| || | || | ||:| || | ||:| | ||:|
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

Qy     196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
      | ||:| || | :|||:| ||:|:|:| || | || ||||| ||||:| :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTA KMLMVVLLV 306
      | || | || | | ||:| ||:| |||||:| |||||
Db     264 RKWK-----PLQPVSQPRGPGQPTKSRMGAVAAEIKQIRARRKTARMLMVVLLV 312

Qy     307 FALCYLFISVLNVLKRVFGMFRQASDREAVYACFTF SHWL VYANSAANPIIYNFLSG 363
      ||:|||||:| ||||| || | ||||| ||||| ||||| |||||
Db     313 FAICYLPISILNVLKRVFGMFAHTEDRET VYAWFTF SHWL VYANSAANPIIYNFLSG 369

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RESULT 15
US-08-513-974B-54
; Sequence 54, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki

```


; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:42:40 ; Search time 19.6209 Seconds
(without alignments)
1809.496 Million cell updates/sec

Title: US-10-070-532-4
Perfect score: 1937
Sequence: 1 MEPSATPGAQMGPVPGSREP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	422.5	21.8	449	2	A41738	neuropeptide Y rec
2	411.5	21.2	370	1	I52315	G protein-coupled
3	392	20.2	381	2	I39187	neuropeptide Y/pep
4	392	20.2	427	2	S50150	gastric CCK-A rece
5	388	20.0	584	2	JC7809	sulfakinin recepto
6	385.5	19.9	519	2	S17783	tachykinin recepto
7	384.5	19.9	452	2	A34916	neurokinin 3 recep
8	384	19.8	465	1	JQ1517	neurokinin 3 recep
9	378.5	19.5	385	2	S55524	neurokinin 3 recep
10	374.5	19.3	428	2	JN0692	cholecystokinin ty
11	373.5	19.3	452	2	JC2459	gastrin/cholecysto
12	371.5	19.2	450	2	JQ1614	gastrin receptor -
13	371	19.2	349	2	I59336	galanin receptor 1

14	370.5	19.1	430	2	I51898	cholecystokinin A
15	370.5	19.1	440	2	A44081	kappa-type opioid
16	370.5	19.1	452	2	A46195	cholecystokinin B
17	367.5	19.0	402	2	I56595	neurokinin 2 recep
18	367	18.9	447	2	A47430	gastrin/cholecysto
19	365.5	18.9	384	1	S00516	neurokinin 2 recep
20	365.5	18.9	398	1	JQ1059	neurokinin 2 recep
21	364.5	18.8	423	2	B40470	glucocorticoid-ind
22	363.5	18.8	387	2	JC5949	galanin receptor 2
23	362	18.7	366	2	S71152	neuropeptide Y/pep
24	362	18.7	444	2	A42685	cholecystokinin re
25	360	18.6	453	2	S32817	gastrin receptor -
26	359.5	18.6	384	2	I57957	neurokinin 2 recep
27	358.5	18.5	390	2	A36737	neurokinin 2 recep
28	356.5	18.4	407	2	S23510	neurokinin 1 recep
29	354.5	18.3	407	1	JQ1274	neurokinin 1 recep
30	352.5	18.2	480	2	I53053	beta 1 adrenergic
31	352	18.2	423	2	JC7677	allatostatin recep
32	351.5	18.1	407	2	A34357	neurokinin 1 recep
33	351	18.1	394	2	JC7209	galanin receptor -
34	351	18.1	477	1	QRHUB1	beta-1-adrenergic
35	350.5	18.1	407	2	S20304	neurokinin 1 recep
36	349.5	18.0	436	2	JC5599	cholecystokinin-A
37	346.5	17.9	384	2	S20303	neurokinin 2 recep
38	346.5	17.9	443	2	D40470	glucocorticoid-ind
39	346.5	17.9	504	2	A41783	tachykinin recepto
40	345	17.8	390	2	B41007	bombesin receptor,
41	340	17.6	483	2	A25896	beta-adrenergic re
42	338.5	17.5	466	2	S36794	beta-1-adrenergic
43	337	17.4	464	2	S12591	beta-1-adrenergic
44	336	17.3	398	2	JN0708	thyrotropin-releas
45	336	17.3	411	2	I56444	thyrotrophin-relea

ALIGNMENTS

RESULT 1

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: UNIPROT:P25931; GB:M81490; NID:g157996; PIDN:AAA28727.1;

PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 21.8%; Score 422.5; DB 2; Length 449;
Best Local Similarity 30.4%; Pred. No. 1e-28;
Matches 105; Conservative 59; Mismatches 126; Indels 55; Gaps 9;

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Qy      26 DYEDFLRLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFI 85
      ||:      | |      :: ::      | : :: ||: ||      | |      ||| ||| ||
Db      75 DYD-----LLSEDMWSSAYFKIIVYMLYIPIFIFALIGNGTVCYIVYSTPRMRTVTNYFI 129

Qy      86 VNLSLADVLVTAICLPASLL-VDITESWLFGHALCKVIPYLQAVSVSAVLTLSFIPLDR 144
      :|:: |::: | |:: | : | | | | | | | | | | | | | | | | | | | | | |
Db     130 ASLAIGDILMSFFCEPSSFISLFILNYWPFGLALCHFVNYSQAVSVLVSAYTLVAISIDR 189

Qy     145 WYAICHPLLEFKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPELANRTRLES-LCH 203
      : | | | | : | | | | | | | | | | | | | | | | | | | | | | |
Db     190 YIAIMWPLKPRITKRYATFIIAGVWFIALATALPIPIV--SGLDIPMSPWHTKCEKYICR 247

Qy     204 ERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPD 263
      | |      | |      | : :: |||:: | : | : | : | |      : |
Db     248 EMWPSRSQEYYYTSLFALQFVVLPLGVLIIFTYARITIRVWAKRPPGEA-----ETNRD 300

Qy     264 QLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRV 323
      |      : |::|| ||:: |::|| |::|| ::| : |
Db     301 Q-----RMASKRKMVKMMLTVVIVFTCCWLPFNILQLL--- 334

Qy     324 FGMFRQASDREAV-----YACFTFSHWLVYANSAANPIIYNFLS 362
      : | |      | | | || | : : | | | | : :
Db     335 -----LNDEEFAHWDPDPYVWFAF-HWLAMSHCCYNPIIYCYMN 372
```

RESULT 2

I52315

G protein-coupled receptor UHR-1 - rat

C;Species: Rattus sp. (rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000

C;Accession: I52315

R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995

A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.

A;Reference number: I52315; MUID:95251659; PMID:7733930

A;Accession: I52315

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-370 <RES>

A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528

C;Superfamily: neurokinin 1 receptor

Query Match 21.2%; Score 411.5; DB 1; Length 370;
Best Local Similarity 30.9%; Pred. No. 7.5e-28;
Matches 99; Conservative 62; Mismatches 118; Indels 41; Gaps 5;

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Qy      44 QYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPAS 103
      | : ::: | | || ||| | : | : | : |||: | ||::|||: | |::|
Db      58 QLKGLIVMLYSIVVVVGLVGNCLLVLVIARVRLHNVTNFLIGNLALSVDVLMCAACVPLT 117
```

Qy 104 LLVDI-TESWLFHALCKVIPYLQAVSVSAVLTLTSFIPLDRWYAICHPLLFKSTARRAR 162
| :|| || :: :|| |:| |:| ||: | :||: : ||| : : : :
Db 118 LAYAFEPRGWVFGGGLCHLVFFLQPVTVYVSVFTLTITIAVDRYVVLVHPLRRRISLKLSA 177

Qy 163 GSILGIWAVSLAIMVPQAAMVQSSSVLPELANRTRLFSLCHERW-ADDLYPKIYHSCFFI 221
::|||::| : :| | : | || | | : : :|| :
Db 178 YAVLGIWALSAVLALPAAVHTYHVELKPHDVR-----LCEEFWGSQERQRIYAWGLLL 231

Qy 222 VTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGR 281
||| || : ::| :: || | :||: : :| |
Db 232 GTYLLPLLAILLSYVRVSVKLRNVRVPGSVTQSQADWDR----- 270

Qy 282 AFLAEVKQMRARRKTAKMLMVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFT 341
||:| :||::|||::||: : |:| : :| | |
Db 271 -----ARRRRTFCLLVVVVVVFALCWLPLHIFNLLR---DLDPRAIDPYAFGLVQL 318

Qy 342 FSHWLVIYANSAANPIIYNFL 361
||| ::| || || :|
Db 319 LCHWLMSSACYNPFIYAWL 338

RESULT 3

I39187

neuropeptide Y/peptide YY receptor Y2 - human

N;Alternate names: neuropeptide y/peptide YY receptor type 2

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: I39187; I39163; G02301

R;Gerald, C.; Walker, M.W.; Vaysse, P.J.

J. Biol. Chem. 270, 26758-26761, 1995

A;Title: Expression cloning and pharmacological characterization of a human hippocampal neuropeptide Y/peptide YY Y2 receptor subtype.

A;Reference number: I39187; MUID:96070760; PMID:7592910

A;Accession: I39187

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-381 <GER>

A;Cross-references: UNIPROT:P49146; EMBL:U36269; NID:g1063633; PIDN:AAC50281.1; PID:g1063634

R;Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kienzle, B.; Seethala, R.

J. Biol. Chem. 270, 22661-22664, 1995

A;Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptide Y receptor.

A;Reference number: I39163; MUID:96032678; PMID:7559383

A;Accession: I39163

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-133,'A',135-381 <ROS>

A;Cross-references: EMBL:U32500; NID:g1000750; PIDN:AAA93170.1; PID:g1000751

R;Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.

submitted to the EMBL Data Library, December 1995

A;Reference number: H01019

A;Accession: G02301

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
A;Cross-references: EMBL:U42389; NID:gl314329; PIDN:AAB07760.1; PID:gl314330
C;Genetics:
A;Gene: GDB:NPY2R
A;Cross-references: GDB:4365607; OMIM:162642
A;Map position: 4q31-4q31
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester bond; transmembrane protein
F;49-76/Domain: transmembrane #status predicted <TM1>
F;87-113/Domain: transmembrane #status predicted <TM2>
F;166-186/Domain: transmembrane #status predicted <TM4>
F;221-237/Domain: transmembrane #status predicted <TM5>
F;269-291/Domain: transmembrane #status predicted <TM6>
F;305-328/Domain: transmembrane #status predicted <TM7>
F;123-203/Disulfide bonds: #status predicted
F;342/Binding site: palmitate (Cys) (covalent) #status predicted
F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.2%; Score 392; DB 2; Length 381;
Best Local Similarity 27.6%; Pred. No. 3.7e-26;
Matches 101; Conservative 70; Mismatches 129; Indels 66; Gaps 9;

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Qy      3 PSATPGAQMVGPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVALV 62
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Db     24 PQTTPRGEL-----VPDPEPELI-----DSTKLIEVQVVLILAYCSIILLGVI 66

Qy     63 GNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCKVI 122
      ||:| | : |||||:| ||:|:|:| | :| | : | | || ::
Db     67 GNSLVIHVVIKFSMRTVTNFFIANLAVADLLVNTLCLPFTLTITLMGEWKMGVPLCHLV 126

Qy    123 PYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGI-WAVSLAIMVPQAA 181
      || | ::| | : :|: | || | : | | :| | :|: | : | : | |
Db    127 PYAQGLAVQVSTITLTVIALDRHRCIVYHLESK-ISKRISFLIIGLAWGISALLASPLAI 185

Qy    182 VMQSS--SVLPELANRTRFLSLCHERWADD---LYPKIYHSCFFIVTYLAPLGLMAMAYF 236
      : | ::| : ||:| : :| :| : : | : |||::: :|
Db    186 FREYSLIEIIPDFE-----IVACTEKWPGEKSIYGTVYSLSSLLILYVLPGLIISFSYT 240

Qy    237 QIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKT 296
      :|: || ||      | | :      | | :      | : ||
Db    241 RIWSKLNKHNHVSPPGA-----ANDHYHQRQRKT 266

Qy    297 AKMLMVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPI 356
      |||: |::|:|: || | : : : | | :      || | : : : |||:
Db    267 TKMLVCVVVFAVSWLP---LHAFQLAVDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPL 323

Qy    357 IYNFLS 362
      :| ::
Db    324 LYGWMN 329

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RESULT 4

S50150

gastric CCK-A receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
 C;Accession: S50150
 R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
 Biochim. Biophys. Acta 1219, 321-327, 1994
 A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.
 A;Reference number: S50150; MUID:95002144; PMID:7918628
 A;Accession: S50150
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-427 <REU>
 C;Superfamily: neurokinin 1 receptor

Query Match 20.2%; Score 392; DB 2; Length 427;
 Best Local Similarity 28.8%; Pred. No. 4.2e-26;
 Matches 110; Conservative 78; Mismatches 150; Indels 44; Gaps 11;

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Qy      8 GAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGN 64
      |  |||      |  ::| | | :  |  ||  | |  | :|:::|
Db      9 GNASGIPP-----PCELGLDNETLFLCLDQP---PPSKEWQPAVQILLYSLIFLLSVLGN 59

Qy     65 TLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPY 124
      |||  : ||  ||||| |::|::|::|  |::|::|::|::| |
Db     60 TLVITVLI RNKRMRTVTNIFLLSLAISDLMLCLFCMPFNLI PNLLKDFIFGSALCKTTTY 119

Qy    125 LQAVSVSVAVLTLSEFIPLDRWYAICHPLLFK--STARRARGSILGIWAVSLAIMVPQAAV 182
      |  |||: | |  |::| || | :  |  |  |  | :| || |
Db    120 LMGTSVSVSTLNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFAIMTPYPIY 179

Qy    183 MQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKL 242
      |::|      : ::|  |: :::|  :::| | :| :| | :|
Db    180 ---SNLVPFTKTNNQTANMCRFLPSDVMQQAHTFLLLLIFLIPGIVMMVAYGMISLEL 236

Qy    243 W-GRQIPGTTSALVRNWK-----RPSDQLGDLEQGLSGEPQPRGRA 282
      : | :  :  : |  :|: || :|:| || |  |
Db    237 YQGIKFDASQKKS AKERKASTGSGRFEDNDGCYLQRSKPTRQL-ELQQ-LSGGGGGRVSR 294

Qy    283 F--LAEVKQMRARRKTAKMLMVVLVFAICYLPISVLNVLKR VFGMFRQASDREAVYACF 340
      :  : |::: :|||:::| ||::| | :  :  :::|
Db    295 IHSSSSAAALMAKKRVIRMLMVIVLFFLCWMPIFSANAWRAYDTV---SAERRLSGTPI 351

Qy    341 TFSHWLVYANSAANPIIYNFLS 362
      :|  | | :|  |||| |::
Db    352 SFILLLSYTSSCVNPIIYCFMN 373
  
```

RESULT 5

JC7809

sulfakinin receptor protein, DSK-R1 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C;Accession: JC7809

R;Kubiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.;

Zantello, M.R.; Lowery, D.E.

Biochem. Biophys. Res. Commun. 291, 313-320, 2002

A;Title: Cloning and functional expression of the first *Drosophila melanogaster* sulfakinin receptor DSK-R1.

A;Reference number: JC7809; PMID:11846406; MUID:21835488

tachykinin receptor homolog DTKR - fruit fly (*Drosophila melanogaster*)
 C;Species: *Drosophila melanogaster*
 C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
 C;Accession: S17783
 R;Li, X.J.; Wolfgang, W.; Wu, Y.N.; North, R.A.; Forte, M.
 EMBO J. 10, 3221-3229, 1991
 A;Title: Cloning, heterologous expression and developmental regulation of a *Drosophila* receptor for tachykinin-like peptides.
 A;Reference number: S17783; MUID:92007772; PMID:1717263
 A;Accession: S17783
 A;Molecule type: mRNA
 A;Residues: 1-519 <LIX>
 A;Cross-references: UNIPROT:P30975; EMBL:X62711; NID:g8505; PIDN:CAA44595.1; PID:g8506
 A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in lacking 481-Gly
 C;Genetics:
 A;Gene: FlyBase:Takr99D
 A;Cross-references: FlyBase:FBgn0004622
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; neurotransmitter receptor; transmembrane protein

Query Match 19.9%; Score 385.5; DB 2; Length 519;
 Best Local Similarity 27.1%; Pred. No. 1.9e-25;
 Matches 105; Conservative 64; Mismatches 145; Indels 73; Gaps 10;

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Qy      3 PSATPGAQMGVPPGSREPS-----PVPPDYED-----EFLRYLWRDYLY 41
      | |      || | |      | | ||      | : || |
Db      45 PCRTLARSSPYPPVSFNHSQTLSTDQPAVGDVEDAEDAAASMETGSFAFVVPWWRQVL- 103

Qy      42 PKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLP 101
      | :: : : :|| || :| | ||||| |||||:| :|:: :
Db      104 -----WSIL--FGGMVIVATGGNLIVVWIVMTTKRMRTVTNYFIVNLSIADAMVSSLNVT 156

Qy      102 ASLLVDITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRA 161
      : : | || ||: :: :|: :| || | :||: || || : : |
Db      157 FNYYYMLDSDWPFGEFYCKLSQFIAMLSICASVFTLMAISIDRYVAIIRPLQPRMSKRCN 216

Qy      162 RGSILGIWAVSLAIMVPQAAVMQSSSV-LPELANRTRLFSLCHERWAD-----DLYPKIY 215
      || | | | : :: | : |:||| :|: | | :|
Db      217 LAIAAVIWLASTLISCPMMIYRTEEVPRGLSNRT----VCYPEWPDGPTNHSTMESLY 272

Qy      216 HSCFFIVTYLAPLGLMAMAYFQIFRWLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGE 275
      : :|| | : | : | :: :||| : ||
Db      273 NILIIILTYFLPIVSMTVTYSRVGIELWGSK-----TIGE 307

Qy      276 PQPRGRAFLAEVKQMRARRKTAKMLMVLLVLFALCYLPISVLNVLKRVFQGMFRQASDREA 335
      || :|: :|::|: ||::||:|:|:|:| : : : :| :
Db      308 CTPR-----QVENVRSKRRVVKMMIVVVLIFAICWLPFHSYFIITSCYPAITEAPFIQE 361

Qy      336 VYACFTFSHWLVYANSAANPIIYNFLS 362
      :| :|| :|| ||||| ::
Db      362 LYLAI---YWLAMSNSMYNPIIYCWMN 385

```

RESULT 7

A34916
 neurokinin 3 receptor - rat
 N;Alternate names: neuromedin K receptor; NK-3 receptor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
 C;Accession: A34916
 R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.
 J. Biol. Chem. 265, 623-628, 1990
 A;Title: Cloning and expression of a rat neuromedin K receptor cDNA.
 A;Reference number: A34916; MUID:90110113; PMID:2153106
 A;Accession: A34916
 A;Molecule type: mRNA
 A;Residues: 1-452 <SHI>
 A;Cross-references: UNIPROT:P16177; GB:J05189; NID:g205670; PIDN:AAA41688.1;
 PID:g205671
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 19.9%; Score 384.5; DB 2; Length 452;
 Best Local Similarity 28.2%; Pred. No. 2e-25;
 Matches 99; Conservative 64; Mismatches 133; Indels 55; Gaps 9;

```

Qy      11 MGVPFGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLA 70
      :|:|  :: || | :  ::|:  || |  | | || | ||: || :|
Db      45 LGLPATTQAPSQVRANLTNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIVIWI 96

Qy      71 VWRNHMMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFHALCKVIPYLQAVSV 130
      :  :  ||| |||: |||: :| | |  :  :  :  | ||  |:  :  :|
Db      97 ILAHKRMRTVTNYFLVNLAFSVASAFAFNTLINFIYGLHSEWYFGANYCRFQNFPPITAV 156

Qy     131 SVAVLTLFSFIPLDRWYAICHPLLEKSTARRARGSILGIWAVSLAIMVPQAAMQSSSVLP 190
      :: ::| :||: || || : :| : | || :: : || :  |:|
Db     157 FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQ-CLYSKIKVMP 215

Qy     191 ELANRTRLFSLCHERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQI 247
      ||  ||: :| :  ||  ||  |: | || :| : | :  ||| :|
Db     216 ---GRT----LCYVQWPEG--PKQHFTYHIIIVILVYCFPLLIMGVITYTIVGITLWGGEI 266

Qy     248 PGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVF 307
      || |  :|:|: || ||::|:|  |
Db     267 PGDTCDKYH-----EQLKAKRKVVKMMIIVVVT 295

Qy     308 ALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358
      |:|:| | :| :  :  : ||  | || ::| |||
Db     296 AICWLPYHVYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSSTMYNPIIY 343

```

RESULT 8

JQ1517

neurokinin 3 receptor - human
 N;Alternate names: neuromedin K receptor; NK-3 receptor
 C;Species: Homo sapiens (man)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
 C;Accession: JQ1517; S20435; S21237
 R;Huang, R.R.C.; Cheung, A.H.; Mazina, K.E.; Strader, C.D.; Fong, T.M.
 Biochem. Biophys. Res. Commun. 184, 966-972, 1992

A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.
 A;Reference number: JQ1517; MUID:92246993; PMID:1374246
 A;Accession: JQ1517
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-465 <HUA>
 A;Cross-references: UNIPROT:P29371; GB:M89473; NID:g189223; PIDN:AAA36366.1; PID:g189224
 A;Experimental source: brain
 R;Buell, G.; Schulz, M.F.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talabot, F.; Kawashima, E.
 FEBS Lett. 299, 90-95, 1992
 A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 receptor.
 A;Reference number: S20435; MUID:92183914; PMID:1312036
 A;Accession: S20435
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2,'I',4-62,'R',64-465 <BUE>
 A;Cross-references: GB:S86392; NID:g246908; PIDN:AAB21706.1; PID:g246909
 R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
 Eur. J. Biochem. 204, 1025-1033, 1992
 A;Title: The primary structure and gene organization of human substance P and neuromedin K receptors.
 A;Reference number: S21188; MUID:92201186; PMID:1312928
 A;Accession: S21237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-438,'F',440-465 <TAK>
 A;Cross-references: GB:X65172; NID:g35022; PIDN:CAA46291.1; PID:g825695
 C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromedin K), one of the peptides in the mammalian tachykinin system.
 C;Genetics:
 A;Gene: GDB:TACR3
 A;Cross-references: GDB:9599126
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
 F;83-111/Domain: transmembrane #status predicted <TM1>
 F;122-147/Domain: transmembrane #status predicted <TM2>
 F;160-181/Domain: transmembrane #status predicted <TM3>
 F;202-221/Domain: transmembrane #status predicted <TM4>
 F;247-272/Domain: transmembrane #status predicted <TM5>
 F;300-321/Domain: transmembrane #status predicted <TM6>
 F;333-355/Domain: transmembrane #status predicted <TM7>
 F;23,50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;158-233/Disulfide bonds: #status predicted

 Query Match 19.8%; Score 384; DB 1; Length 465;
 Best Local Similarity 27.9%; Pred. No. 2.3e-25;
 Matches 100; Conservative 67; Mismatches 135; Indels 56; Gaps 10;

 Qy 4 SATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVALVG 63
 |::| |::| | || : :::: || | | || |:::|
 Db 52 SSSPSA-LGLPVASAPSPQWANLTNQFVQPSWRIAL-----WSL--AYGVVVAVAVLG 102

Qy 64 NTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIP 123
 | : | : : | | | | | : | : | : : | | | :
 Db 103 NLIVIWII LAHKRMRTVTNYFLVNLA FSDASMAAFNTLVNFIYALHSEWYFGANYCRFQN 162

Qy 124 YLQAVSVSVAVLTL SFIP LDRWYAICHPLL FFKSTARRARGSILGIWAVSLAIMVPQAAM 183
 : : | : : : : | : | : | | : : | | : : | :
 Db 163 FFPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQ-CLY 221

Qy 184 QSSSVLP ELANRTRLFSLCHERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 : | : | | | : | : | | | : | | : | : | :
 Db 222 SKTKVMP---GRT----LCFVQWPEG--PKQHFTYHIIIVII LVYCFPLLIMGITYTIVGI 272

Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 | | | : | | | : | : | : | : | : | : | : | :
 Db 273 TLWGGEIPGDTCDKYH-----EQLKAKRKVVKMM 301

Qy 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358
 : : | : | : | : | : | : | : | : | : | : | : | :
 Db 302 IIVVMTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLA----SFWLAMSSMTMYNPIIY 356

RESULT 9

S55524

neurokinin 3 receptor - mouse (fragment)

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Mus musculus (house mouse)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S55524; I73045

R;Maroteaux, L.

submitted to the EMBL Data Library, June 1995

A;Reference number: S55524

A;Accession: S55524

A;Molecule type: mRNA

A;Residues: 1-385 <MAR>

A;Cross-references: UNIPROT:P47937; EMBL:X87823; NID:g861055; PIDN:CAA61088.1; PID:g861056

R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.; Weinstock, J.V.

J. Immunol. 152, 1830-1835, 1994

A;Title: Molecular evidence that granuloma T lymphocytes in murine schistosomiasis mansoni express an authentic substance P (NK-1) receptor.

A;Reference number: I56216; MUID:94165478; PMID:8120392

A;Accession: I73045

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 103-197, 'S', 199-266, 'P', 268-328 <OOO>

A;Cross-references: GB:L27827; NID:g450288; PIDN:AAA17893.1; PID:g480780

C;Superfamily: neurokinin 1 receptor

Query Match 19.5%; Score 378.5; DB 2; Length 385;
 Best Local Similarity 28.2%; Pred. No. 5.5e-25;
 Matches 99; Conservative 63; Mismatches 134; Indels 55; Gaps 9;

Qy 11 MGVP PGSPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLA 70
 : | : | : | : : | : | | | | | | : | : | : | :
 Db 45 LGLPVTSQAPSQVRDNL TNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIWI 96

Qy 71 VWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSV 130
: : |||||:|:| :| : : : || : : :|
Db 97 ILAHKRMRTVTNYFLVNLAFSVASAFNTLVNFIYGVHSEWYFGANYCRFQNFPPITAV 156

Qy 131 SVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQAAMQSSSVLP 190
: : : : | :|: || || : :| : | || : : || : :|
Db 157 FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQ-CLYSKIKVMP 215

Qy 191 ELANRTRLFSLCHERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQI 247
|| ||: :| : || || :| || :| :| : || :|
Db 216 ---GRT---LCYVQWPEG--PKQHFTYHIIIVILVYCFPLLIMGVTYTIVGITLWGGEI 266

Qy 248 PGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVF 307
| | :|:|:| || :|:|:|
Db 267 LGDTCDKYH-----EQLKAKRKVVKMMIIVVTF 295

Qy 308 ALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIY 358
|:|:| | :| : : : || | || : : ||||
Db 296 AICWLPYHVYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSTMYNPIIY 343

RESULT 10

JN0692

cholecystokinin type A receptor - human

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: JN0692; JN0590

R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.

Biochem. Biophys. Res. Commun. 194, 811-818, 1993

A;Title: Molecular cloning, functional expression and chromosomal localization of the human cholecystokinin type A receptor.

A;Reference number: JN0692; MUID:93343941; PMID:8343165

A;Accession: JN0692

A;Molecule type: mRNA

A;Residues: 1-428 <DEW>

A;Cross-references: UNIPROT:P32238; GB:L19315; NID:g306595; PIDN:AAA02819.1;

PID:g306596

A;Experimental source: gallbladder

R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.

Biochem. Biophys. Res. Commun. 193, 204-211, 1993

A;Title: Molecular cloning and functional expression of the human gallbladder cholecystokinin A receptor.

A;Reference number: JN0590; MUID:93277552; PMID:8503909

A;Accession: JN0590

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-428 <ULR>

A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491

A;Experimental source: gallbladder

C;Comment: This protein has diverse physiological roles in the gastrointestinal system where it mediates pancreatic growth and enzyme secretion, smooth muscle contraction of the gallbladder and stomach, and secretion from gastric mucosal cells.

C;Genetics:

A;Gene: GDB:CCKAR

A;Cross-references: GDB:141927; OMIM:118444

A;Map position: 4pter-4qter

C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
 phosphoprotein; transmembrane protein
 F;40-67/Domain: transmembrane #status predicted <TM1>
 F;78-104/Domain: transmembrane #status predicted <TM2>
 F;116-137/Domain: transmembrane #status predicted <TM3>
 F;158-178/Domain: transmembrane #status predicted <TM4>
 F;208-234/Domain: transmembrane #status predicted <TM5>
 F;314-332/Domain: transmembrane #status predicted <TM6>
 F;350-369/Domain: transmembrane #status predicted <TM7>
 F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase C)
 #status predicted
 F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status
 predicted

Query Match 19.3%; Score 374.5; DB 2; Length 428;
 Best Local Similarity 28.3%; Pred. No. 1.4e-24;
 Matches 106; Conservative 76; Mismatches 155; Indels 37; Gaps 10;

```

Qy      16 GSREPSVPDPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGNTLVCLAVW 72
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      11 GSNITPPCELGLENETLFLCL--DQPRPSK-EWQPAVQILLYSLIFLLSVLGNTLVITVLI 67

Qy      73 RNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCKVIPYLQAVSVSV 132
      ||  |||||  |::|::|::|  |:  |:  ::  :  ::||  |::|  |  ||||
Db      68 RNKRMRTVTNIFLLSLAVSDMLCLFCMPFNLPNLLKDFIFGSAVCKTTTYFMGTSVSV 127

Qy     133 AVLTLSFIPLDRWYAICHPLLFK--STARRAGSILGIWAVSLAIMVPQAAMQSSSVLP 190
      :  |  |  |::|  ||  |  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     128 STFNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFTIMTPYPIY---SNLVP 184

Qy     191 ELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLW----- 243
      |  :  ::|  :|:  :  ::  ::  :|  |  :|  :||  |  :|:
Db     185 FTKNNNQNTANMCRFLPNVDVMQQSWHTFLLILFLIPGIVMMVAYGLISLELYQGIKFEA 244

Qy     244 -----GRQIPGTTSA-----LVRNWKRPDQLGDLEQGLSGEPQPRGR-AFLAEVK 288
      :  |  |||:  ||  :|  :|  |  :|  |  |  :
Db     245 SQKKSAKERKPKSTTSSGKYEDSDGCYLQKTRPPRKL-ELRQLSTGSSSRANRIRSNSAA 303

Qy     289 QMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVY 348
      :  |::  :||:|:::|  ||::||  |  :  ::|  :|  |  |
Db     304 NLMAKKRVIRMLIVIVLFFLCWMPIFSANAWR---AYDTASAERRLSGTPISFILLLSY 360

Qy     349 ANSAANPIIYNFLS 362
      :|  ||||  |::
Db     361 TSSCVNPIIYCFMN 374

```

RESULT 11

JC2459

gastrin/cholecystokinin B receptor - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: JC2459

R;Blandizzi, C.; Song, I.; Yamada, T.

Biochem. Biophys. Res. Commun. 202, 947-953, 1994

A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor gene.

A;Reference number: JC2459; MUID:94324990; PMID:8048969

A;Accession: JC2459

A;Molecule type: mRNA

A;Residues: 1-452 <BLA>

A;Cross-references: UNIPROT:P46627; GB:L31548; NID:g495663; PIDN:AAA31194.1;

PID:g495665

C;Genetics:

A;Introns: 49/1; 133/1; 216/2; 273/1

C;Superfamily: neurokinin 1 receptor

C;Keywords: receptor; transmembrane protein

F;56-79/Domain: transmembrane #status predicted <TM1>

F;85-104/Domain: transmembrane #status predicted <TM2>

F;130-149/Domain: transmembrane #status predicted <TM3>

F;169-187/Domain: transmembrane #status predicted <TM4>

F;217-237/Domain: transmembrane #status predicted <TM5>

F;339-359/Domain: transmembrane #status predicted <TM6>

F;381-400/Domain: transmembrane #status predicted <TM7>

Query Match 19.3%; Score 373.5; DB 2; Length 452;

Best Local Similarity 27.0%; Pred. No. 1.8e-24;

Matches 99; Conservative 69; Mismatches 124; Indels 75; Gaps 9;

```
Qy      48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
      : : | :|::: || |: : : : :| ||| |::|::|::|: | :| :| :
Db      54 IRVTLYAVIFLMSVGGNIIIVVLGLSRRLRTVTNAFLLSLAVSDLLAVACMPFTLLPN 113

Qy      108 ITESWLFGHALCKVIPYQLQAVSVSVAVLTLSFIPLDRWYAICHPLLFK--STARRARGSI 165
      : :::|| :|| : || ||||: |:| | |:|: ||| || : | | |
Db      114 LMGTFIFGTVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARVI 173

Qy      166 LGIWAWSLAIMVPQAAVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYL 225
      | | :| :||| | | : | || : : : :
Db      174 LATWLLSGLLMVPYPVYTAVQPVGPRVLQ-----CVHRWPSARVRQTWSVLLLLLLFF 226

Qy      226 APLGLMAMAYFQIFRKLW-----GRQIPGTTSALVRNWKRP 261
      | :||:| | |:| : | || |
Db      227 VPGVMAVAYGLISRELYLGLRFDSDSDSESQSRVRGQGLPGGAAPG-----P 275

Qy      262 SDQLGDL--EQGLSGE-----PQPRGRAFL-----AEVKQMRARR 294
      | | | ||:| | || | | | | : | : | :
Db      276 VHQNGRCRPEAGLAGEDGDGCYVQLPRSRPALELSALTAPISGPGGPRPAQAK--LLAKK 334

Qy      295 KTAKMLMVLLVLFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAAN 354
      : :||:|:::| :|:|: | : | : | | :| | | | : |
Db      335 RVVRMLLVIVVLFFMCWLPVYSANTWRAFDG---PGAHRALSGAPISFIHLLSYASACVN 391

Qy      355 PIYNFL 361
      |::| |:
Db      392 PLVYCFM 398
```

RESULT 12

JQ1614

gastrin receptor - multimammate rat (Mastomys natalensis)

C;Species: Mastomys natalensis

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C;Accession: JQ1614
 R;Nakata, H.; Matsui, T.; Ito, M.; Taniguchi, T.; Naribayashi, Y.; Arima, N.;
 Nakamura, A.; Kinoshita, Y.; Chihara, K.; Hosoda, S.; Chiba, T.
 Biochem. Biophys. Res. Commun. 187, 1151-1157, 1992
 A;Title: Cloning and characterization of gastrin receptor from ECL carcinoid
 tumor of *Mastomys natalensis*.
 A;Reference number: JQ1614; MUID:92412082; PMID:1530611
 A;Accession: JQ1614
 A;Molecule type: mRNA
 A;Residues: 1-450 <NAK>
 A;Cross-references: UNIPROT:P30796; GB:D12817; NID:g220646; PIDN:BAA02250.1;
 PID:g220647
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor;
 transmembrane protein
 F;59-83/Domain: transmembrane #status predicted <TM1>
 F;87-109/Domain: transmembrane #status predicted <TM2>
 F;132-150/Domain: transmembrane #status predicted <TM3>
 F;172-188/Domain: transmembrane #status predicted <TM4>
 F;216-243/Domain: transmembrane #status predicted <TM5>
 F;334-357/Domain: transmembrane #status predicted <TM6>
 F;380-398/Domain: transmembrane #status predicted <TM7>
 F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2%; Score 371.5; DB 2; Length 450;
 Best Local Similarity 28.8%; Pred. No. 2.6e-24;
 Matches 101; Conservative 67; Mismatches 136; Indels 47; Gaps 9;

```

Qy      48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
      : | | :|::: || | : : : : |||| |::|::|::|: | :| :| :
Db      56 IRITLYAVIFLMSIGGNMLIIVVLGLSRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLPN 115

Qy      108 ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFK--STARRARGSI 165
      : ::|| :|| : || ||||: | | | |:| || | | : | | |
Db      116 LMGTFIFGTVICKAVSYLMGVSVSVSTLNLVAIALERYSAICRPLQARVWQTRSHAARVI 175

Qy      166 LGIWAVSLAIMVPQAAVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYL 225
      | | :| :|| | | : | | : : : :
Db      176 LATWLLSGLMVPYPVYTVVQPVGPRVLQ-----CMHRWPSARVRQTWSVLLMLLFF 228

Qy      226 APLGLMAMAYFQIFRKLW-GRQIPG----TTSALVRNW-----KRPSDQLGDLEQ-G 271
      | :||:| | |:|: | : | | : || | | |
Db      229 IPGVMAVAYGLISRELYLGLRFDGDNDSDTQSRVRNQGGLPGGTAPGPVHQNGGCRHVT 288

Qy      272 LSGEPQ-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLVFALC 310
      ::|| | | : | : : |:: :|:|::| | |
Db      289 VAGEDNDGCYVQLPRSRLEMTTLTTPTPGPGGLASANQAKLLAKKRVRMLLVIVLLFFLC 348

Qy      311 YLPISVLNVLKRVFQMFQASDREAVYACFTFSHWLVYANSAANPIIYNFL 361
      :|| | | : | | : | | | |:: |::| | :
Db      349 WLPIYSANTWCAFDG---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM 396

```

RESULT 13
 I59336
 galanin receptor 1 - human

C;Species: Homo sapiens (man)
 C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
 C;Accession: I59336; JC5801; G01765; G02528
 R;Habert-Ortoli, E.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994
 A;Title: Molecular cloning of a functional human galanin receptor.
 A;Reference number: I59336; MUID:95024044; PMID:7524088
 A;Accession: I59336
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-349 <HAB>
 A;Cross-references: UNIPROT:P47211; GB:L34339; NID:g559047; PIDN:AAA50767.1;
 PID:g559048
 R;Lorimer, D.D.; Matkowskj, K.; Benya, R.V.
 Biochem. Biophys. Res. Commun. 241, 558-564, 1997
 A;Title: Cloning, chromosomal location, and transcriptional regulation of the
 human galanin-1 receptor gene (GALN1R).
 A;Reference number: JC5801; MUID:98086390; PMID:9425310
 A;Accession: JC5801
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-349 <LOR>
 A;Cross-references: GB:U53511; NID:g1297337; PIDN:AAC51936.1; PID:g1297338
 A;Note: submitted to the EMBL Data Library, April 1996
 R;Ross, P.C.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: G08350
 A;Accession: G01765
 A;Status: translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-14,'W',16-349 <ROS>
 A;Cross-references: EMBL:U23854; NID:g775209; PID:g775210
 C;Comment: This receptor inhibits cAMP formation, stimulates and inhibits
 phospholipase C activity, decreases phorbol ester-induced protein
 phosphorylation by a protein kinase C-independent mechanism, and increases
 arachadonic acid metabolism, as well as opens ATP-dependent K+ but closes N-type
 Ca2+ channels.
 C;Genetics:
 A;Gene: GDB:GALNR
 A;Cross-references: GDB:392699; OMIM:600377
 A;Map position: 18q23-18q23
 C;Superfamily: vertebrate rhodopsin

Query Match 19.2%; Score 371; DB 2; Length 349;
 Best Local Similarity 29.9%; Pred. No. 2.2e-24;
 Matches 97; Conservative 62; Mismatches 107; Indels 58; Gaps 10;

Qy 47 WVLIAAYVAVFVVALVGNTLVCLAVWRNH--HMRTVTNYFIVNLSLADVLVTAICLPASL 104
 :| : : :| : ::||:| : |: | : || :||:| :| :| :|
 Db 34 FVTLLVVFGLIFALGVLGNSLVITVLARSKPGKPRSTTNLFILNLSIADLAYLLFCIPFQA 93
 Qy 105 LVDITESWLFGLHALCKVIPYLQAVSVSAVLTLSFIPLDRWYAICHPLLFKSTARRARGS 164
 | :| :| :||| | ||: |: : ||: : :||: || | :| :| :| :|
 Db 94 TVYALPTWVLGAFICKFIHYFFTVMVLSIFTLAAMSVDYVAIVHSRR-SSSLRVSRNA 152
 Qy 165 ILG---IWAVSLAIMVPOAAVMQSSSVLPPELANRTRFLSLCHERWADDLYPKIYHSCFFI 221
 :|| ||:|:| :| | :|:| | :| :| :| :| :| :| :| :| :| :|

Db 153 LLGVGCIWALSAMASPVA--YHQGLFHPRASNTQ----FCWEQWPDPRHKKAYVVCTFV 206

Qy 222 VTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGR 281
 || || | : | : | : : | : | :

Db 207 FGYLLPLLLICFCYAKVLNHLHKK-----LKNMSKKSE----- 239

Qy 282 AFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFT 341
 : : || | : : || : | : : | : | |

Db 240 -----ASKKKAQTVLVVVVVFGISWLPHHIIH-LWAEFGVF-----PLTPASFL 283

Qy 342 F---SHWLVYANSAANPIIYNFLS 362
 | : | | | : | | | | |

Db 284 FRITAHCLAYSNSSVNPIIYAFLS 307

RESULT 14

I51898

cholecystokinin A receptor - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004

C;Accession: I51898

R;De Weerth, A.; Pisegna, J.R.; Wank, S.A.

Am. J. Physiol. 265, G1116-G1121, 1993

A;Title: Guinea pig gallbladder and pancreas possess identical CCK-A receptor subtypes: receptor cloning and expression.

A;Reference number: I51898; MUID:94106629; PMID:7916580

A;Accession: I51898

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-430 <RES>

A;Cross-references: UNIPROT:Q63931; GB:S68242; NID:g544723; PIDN:AAB29504.1;

PID:g544724

C;Superfamily: neurokinin 1 receptor

Query Match 19.1%; Score 370.5; DB 2; Length 430;

Best Local Similarity 27.4%; Pred. No. 3e-24;

Matches 104; Conservative 77; Mismatches 152; Indels 47; Gaps 10;

Qy 16 GSREPSVPPDYEDFLRYLWRDYLYPK-QYEW--VLIAAYVAVFVVALVGNTLVCLAV 71
 || | : | | | : | | | : | : | : |

Db 11 GSNITSACELGFENETLFCILDR----PRPSKEWQPAVQILLYSLIFLLSVLGNTLVITVL 66

Qy 72 WRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCKVIPYLQAVSVS 131
 || || || || | : : | : : | : | : | : | : |

Db 67 IRNKRMR'TVTNIFLLSLAVSDMLCLFCMPFNLPDLLKDFIFGSAVCKTTTYFMGTSVS 126

Qy 132 VAVLTLSFIPLDRWYAICHPLLEK--STARRARGSILGIWAVSLAIMVPQAQAVMQSSSVL 189
 | : | | | : | : | | | : | | | | : | : |

Db 127 VSTFNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFITIMTPYPIY---SNLV 183

Qy 190 PELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLW-GRQIP 248
 | | : : | : : : : : : : | : | : | : |

Db 184 PFTKNNNQTNMCRFLLENDVMQQTWHTFLLLLILFLIPGIVMMVAYGLISLELYQGIKFD 243

Qy 249 GTTSALVRNWKRPDQLGDLEQG----LSGEPQPRGRAFLAEVKQ----- 289
 : | : | : | | | : |

Db 244 AIQKKSARKERTSTGSSGPMEDSDGCYLQKSRHPR----KLELRQLSPSSSGSNRINRIR 299

Qy 290 -----MRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTF 342
 : |::: :||:|:::| ||:| | : : :::| :|
 Db 300 SSSSTANLMAKKRVIRMLIVIVVLFCLWMPIFSANAWRAYDTV---SAERHLSGTPISF 356
 Qy 343 SHWLVYANSAANPIIYNFLS 362
 | | : | |||| |::
 Db 357 ILLLSYTSSCVNPIIYCFMN 376

RESULT 15

A44081

kappa-type opioid receptor - human

C;Species: Homo sapiens (man)

C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: A44081

R;Xie, G.X.; Miyajima, A.; Goldstein, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 4124-4128, 1992

A;Title: Expression cloning of cDNA encoding a seven-helix receptor from human placenta with affinity for opioid ligands.

A;Reference number: A44081; MUID:92237319; PMID:1315051

A;Accession: A44081

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-440 <XIE>

A;Cross-references: UNIPROT:P30098; GB:M84605; NID:g189391; PIDN:AAA36395.1; PID:g189392

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.1%; Score 370.5; DB 2; Length 440;
 Best Local Similarity 28.3%; Pred. No. 3.1e-24;
 Matches 106; Conservative 59; Mismatches 138; Indels 72; Gaps 12;

Qy 4 SATPGAQMGVPP-----GSREPSVP-----PDYEDEFRLRYLWRDYLPKQ 44
 || || | || : || | | | : | |
 Db 9 SAWPG--WGWPPAALRNLTSSPAPTASPSAPSWTPSPRPGPAHPFLQPPWAVAL---- 62
 Qy 45 YEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASL 104
 | | || || ||::|| : | : |||| |::| : | : :
 Db 63 --WSL--AYGAVVAVAVLGNLVVIWIVLAHKRMRTVTNSFLVNLAFADAAMAALNALVNF 118
 Qy 105 LVDITESWLFHALCKVIPYLAQSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGS 164
 : : | || | : : : | : : : | : | : | : : |
 Db 119 IYALHGEWYFGANYCRFQNFPPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATATRIV 178
 Qy 165 ILGIWAVSLAIMVPQAAMQSSSVLPELANRTRLFSLCHERWADDLYPKI-YHSCFFIVT 223
 | || : : || : | : || || : : | : || : :
 Db 179 IGSIWILAFLLAFPO-CLYSKIKVMP---GRT---LCYVQWPEGSRQHFTYHMIVIVLV 230
 Qy 224 YLAPLGLMAMAYFQIFRKLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAF 283
 | || : | : : || : || | | | | | |
 Db 231 YCFPLLIMGITYTIVGITLWGGEIPGDTC-----DKYQ----- 263
 Qy 284 LAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFS 343
 :||:|:| ||::|:| ||:|:| : : | : : : || |
 Db 264 ----EQLKAKRKVVKMMIIVVVTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLA---S 316

Qy 344 HWLVYANSAANPIIY 358
/ || ::: ||||
Db 317 FWLAMSSTMYNPIIY 331

Search completed: October 14, 2004, 10:56:56
Job time : 21.6209 secs

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:55:56 ; Search time 68.6732 Seconds
(without alignments)
1737.280 Million cell updates/sec

Title: US-10-070-532-4
Perfect score: 1937
Sequence: 1 MEPSATPGAQMVGVPGRREP.....NSAANPLIYNFLSGLPWSLL 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result 8
Query

No.	Score	Match	Length	DB	ID	Description
1	1937	100.0	369	10	US-09-393-696-4	Sequence 4, Appli
2	1909	98.6	369	13	US-10-077-874-4	Sequence 4, Appli
3	1875	96.8	389	9	US-09-828-538-20	Sequence 20, Appl
4	1875	96.8	389	10	US-09-211-823C-23	Sequence 23, Appl
5	1875	96.8	425	9	US-09-828-538-19	Sequence 19, Appl
6	1875	96.8	425	9	US-09-828-538-24	Sequence 24, Appl
7	1875	96.8	425	10	US-09-211-823C-22	Sequence 22, Appl
8	1875	96.8	425	14	US-10-225-567A-368	Sequence 368, App
9	1875	96.8	425	14	US-10-352-684A-22	Sequence 22, Appl
10	1874	96.7	402	10	US-09-393-696-2	Sequence 2, Appli
11	1872	96.6	372	10	US-09-393-696-6	Sequence 6, Appli
12	1872	96.6	372	13	US-10-077-874-6	Sequence 6, Appli
13	1870	96.5	425	10	US-09-826-509-549	Sequence 549, App
14	1869	96.5	402	13	US-10-077-874-2	Sequence 2, Appli
15	1869	96.5	425	9	US-09-961-848-2	Sequence 2, Appli
16	1755	90.6	427	9	US-09-730-931-2	Sequence 2, Appli
17	1326.5	68.5	460	14	US-10-081-810-46	Sequence 46, Appl
18	1313.5	67.8	444	10	US-09-992-331-19	Sequence 19, Appl
19	1313.5	67.8	444	14	US-10-081-810-45	Sequence 45, Appl
20	1313.5	67.8	444	14	US-10-225-567A-370	Sequence 370, App
21	1313.5	67.8	444	14	US-10-262-313-19	Sequence 19, Appl
22	1313.5	67.8	444	14	US-10-060-369-11	Sequence 11, Appl
23	1313.5	67.8	444	14	US-10-178-194-2	Sequence 2, Appli
24	1313.5	67.8	444	16	US-10-768-878-19	Sequence 19, Appl
25	1312.5	67.8	444	14	US-10-282-717-2	Sequence 2, Appli
26	1308.5	67.6	444	10	US-09-826-509-551	Sequence 551, App
27	1279	66.0	263	14	US-10-278-087A-54	Sequence 54, Appl
28	483.5	25.0	430	9	US-09-866-248A-8	Sequence 8, Appli
29	483.5	25.0	430	14	US-10-225-567A-658	Sequence 658, App
30	483.5	25.0	430	16	US-10-719-587-54	Sequence 54, Appl
31	483.5	25.0	441	14	US-10-292-798-890	Sequence 890, App
32	480.5	24.8	432	9	US-09-866-248A-2	Sequence 2, Appli
33	480.5	24.8	432	16	US-10-719-587-37	Sequence 37, Appl
34	479.5	24.8	428	9	US-09-292-973-4	Sequence 4, Appli
35	473.5	24.4	420	9	US-09-866-248A-6	Sequence 6, Appli
36	473.5	24.4	420	14	US-10-060-369-9	Sequence 9, Appli
37	473.5	24.4	522	14	US-10-081-810-53	Sequence 53, Appl
38	473.5	24.4	522	14	US-10-225-567A-512	Sequence 512, App
39	473.5	24.4	522	14	US-10-255-551-2	Sequence 2, Appli
40	473.5	24.4	522	15	US-10-072-012-360	Sequence 360, App
41	473.5	24.4	522	15	US-10-072-012-361	Sequence 361, App
42	473.5	24.4	522	15	US-10-276-774-2093	Sequence 2093, Ap
43	473.5	24.4	522	17	US-10-757-262-8	Sequence 8, Appli
44	467.5	24.1	417	15	US-10-072-012-358	Sequence 358, App
45	453	23.4	426	9	US-09-292-973-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-393-696-4

; Sequence 4, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

```
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-4
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Query Match          100.0%; Score 1937; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.7e-172;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSAVLTLSFIPLDRWYAICHPLLFKSTARRARGSVILGIWAVSLAIMVPQA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSAVLTLSFIPLDRWYAICHPLLFKSTARRARGSVILGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGLPWSLL 369
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Db    361 LSGLPWSLL 369
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RESULT 2
US-10-077-874-4
; Sequence 4, Application US/10077874
; Publication No. US20020115155A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
```



```

; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 369 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-077-874-4

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Query Match          98.6%; Score 1909; DB 13; Length 369;
Best Local Similarity 98.6%; Pred. No. 7.1e-170;
Matches 364; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180
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Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db    181 AVMECSSVLPELANRTRFLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

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Db      301 MVLVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTTFSHWLVYANSAANPIIYNF 360
Qy      361 LSGLPWSLL 369
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Db      361 LSGLPWSLL 369

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RESULT 3

US-09-828-538-20

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; Sequence 20, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-20

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Query Match          96.8%; Score 1875; DB 9; Length 389;
Best Local Similarity 98.6%; Pred. No. 1.1e-166;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
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Db      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

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Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||: |||||:| |||||
 Db 181 AVMECSSVLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||: |||||:| |||||
 Db 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||: |||||:| |||||
 Db 301 MVVLLVFALCYLPISVLNVLRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 389

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-211-823C-23

Query Match 96.8%; Score 1875; DB 10; Length 389;

Best Local Similarity 98.6%; Pred. No. 1.1e-166;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
 |||||: |||||:| |||||

Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 |||||: |||||:| |||||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
 |||||
 Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
 Qy 181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||: |||||:| |||||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLGWRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||
 Db 241 KLGWRQIPGTTSALVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 5

US-09-828-538-19

; Sequence 19, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624

; PRIOR FILING DATE: 1998-06-08

; PRIOR APPLICATION NUMBER: 60/093,726

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: 09/328,014

; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 19

; LENGTH: 425

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-828-538-19

Query Match 96.8%; Score 1875; DB 9; Length 425;

Best Local Similarity 98.6%; Pred. No. 1.3e-166;

Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWLVIAAYVAVFVVA 60

```

Db      1 MEPSATPGAQMGVPPGSRPEPSVPFPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
Qy      121 VIPYLQAVSVSAVLTLFSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180
Db      121 VIPYLQAVSVSAVLTLFSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180
Qy      181 AVMQSSSVLPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db      181 AVMECSSVLPELANRTRFLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy      241 KLWGRQIPGTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db      241 KLWGRQIPGTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy      301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db      301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
Db      361 LSG 363

```

RESULT 6

US-09-828-538-24

; Sequence 24, Application US/09828538

; Patent No. US20010025031A1

; GENERAL INFORMATION:

; APPLICANT: Ellis, Catherine E.

; APPLICANT: Kwok, Cheni

; APPLICANT: Bodsworth, Nicola J.

; APPLICANT: Halsey, Wendy

; APPLICANT: Van Horn, Stephanie

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods

; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications

; FILE REFERENCE: GH-50038-C1

; CURRENT APPLICATION NUMBER: US/09/828,538

; CURRENT FILING DATE: 2001-04-06

; PRIOR APPLICATION NUMBER: 60/088,624

; PRIOR FILING DATE: 1998-06-08

; PRIOR APPLICATION NUMBER: 60/093,726

; PRIOR FILING DATE: 1998-07-22

; PRIOR APPLICATION NUMBER: 09/328,014

; PRIOR FILING DATE: 1999-06-08

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 24

; LENGTH: 425

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-828-538-24

Query Match 96.8%; Score 1875; DB 9; Length 425;
Best Local Similarity 98.6%; Pred. No. 1.3e-166;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||
Db    181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSAIVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSAIVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 7

US-09-211-823C-22

; Sequence 22, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-22

Query Match 96.8%; Score 1875; DB 10; Length 425;
Best Local Similarity 98.6%; Pred. No. 1.3e-166;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMVGPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMVGPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||
Db    181 AVMECSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 8

US-10-225-567A-368
; Sequence 368, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 368
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-368

Query Match 96.8%; Score 1875; DB 14; Length 425;
Best Local Similarity 98.6%; Pred. No. 1.3e-166;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSRFPSVPPDYEDFLRYLWRDYLYPEWVLIAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSRFPSVPPDYEDFLRYLWRDYLYPEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||: |||: |||
Db    181 AVMECSSVLPELANRTRFLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KIWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KIWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVLVLFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
```

RESULT 9

US-10-352-684A-22

; Sequence 22, Application US/10352684A

; Publication No. US20030215452A1

; GENERAL INFORMATION:

; APPLICANT: Millennium Pharmaceuticals Inc.

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; APPLICANT: Weich, Nadine S.

; APPLICANT: Kelly, Louise M.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,

; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,

; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,

; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES

; FILE REFERENCE: MPI02-019P1RNOMNIM

Db 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 10

US-09-393-696-2

; Sequence 2, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-2

Query Match 96.7%; Score 1874; DB 10; Length 402;
Best Local Similarity 98.3%; Pred. No. 1.5e-166;
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
|||||
Db 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIPAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
|||||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180
|||||
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPOA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||: |||||: |||||
Db 181 AVMECSSVLPELANRTRLFVCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||||
Db 241 NLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||||
Db 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||
Db 361 LSG 363

RESULT 11

US-09-393-696-6

; Sequence 6, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-6

Query Match 96.6%; Score 1872; DB 10; Length 372;
Best Local Similarity 98.3%; Pred. No. 2.1e-166;
Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSRPSPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
|||||:|||||
Db 1 MEPSATPGAQMGPVPPGSRDPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTACLPAALLVDITESWLFQHALCK 120
|||||:|||||
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTACLPAALLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
|||||:|||||
Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|||:|||||
Db 181 AVMECSSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|||||:|||||
Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVLLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|||||:|||||
Db 301 MVLLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|||

Db 361 LSG 363

RESULT 12

US-10-077-874-6

; Sequence 6, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 372 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-077-874-6

Query Match 96.6%; Score 1872; DB 13; Length 372;

Best Local Similarity 98.3%; Pred. No. 2.1e-166;

Matches 357; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLKPKQYEWVLI AAYVAVFVVA 60
| | | | | : | | | | |

Db 1 MEPSATPGAQMGVPPGSRDPSVPPDYEDFLRYLWRDYLKPKQYEWVLI AAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
| | | | | : | | | | |

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy	121	VIPYLQAVSVSAVLTLTSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSAVLTLTSFIPLDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTTALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTTALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFHSWLVIYANSAANPIIYNF	360
Db	301	MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFHSWLVIYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

US-09-826-509-549

; Sequence 549, Application US/09826509

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

Known G

```
; TITLE OF INVENTION: Protein-Coupled Receptors
```

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

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; SOFTWARE: PatentIn Version 2.1
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; SEQ ID NO 549

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-549

Best Local Similarity 98.3%; Pred. No. 3.7e-166;

Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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Db 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Db	61	LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTKKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 14

US-10-077-874-2

; Sequence 2, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

```

;           TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;           LENGTH: 402 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-077-874-2

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Query Match          96.5%;   Score 1869;   DB 13;   Length 402;
Best Local Similarity 98.3%;   Pred. No. 4.3e-166;
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
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Db    361 LSG 363

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RESULT 15

US-09-961-848-2

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; Sequence 2, Application US/09961848
; Patent No. US20020146719A1
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-004
; CURRENT APPLICATION NUMBER: US/09/961,848
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/479,128
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083

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; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-961-848-2
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Query Match          96.5%; Score 1869; DB 9; Length 425;
Best Local Similarity 98.3%; Pred. No. 4.6e-166;
Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180

Qy    181 AVMQSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSSVLPPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVLVLLVFALCYLPISVLNVLKRFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
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Search completed: October 14, 2004, 11:16:35
Job time : 69.6732 secs
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:41:50 ; Search time 96.8388 Seconds
(without alignments)
2192.441 Million cell updates/sec

Title: US-10-070-532-4
Perfect score: 1937
Sequence: 1 MEPSATPGAQMGVPPGSRP.....NSAANPIIYNFLSGLPWSLL 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1875	96.8	425	1	OX1R_HUMAN	O43613 homo sapien
2	1869	96.5	425	2	Q9HBV6	Q9hbv6 homo sapien
3	1755	90.6	416	1	OX1R_RAT	P56718 rattus norv
4	1753	90.5	416	2	Q6VNS3	Q6vns3 mus musculu
5	1753	90.5	416	2	AAR01326	Aar01326 mus muscu
6	1326.5	68.5	460	1	OX2R_RAT	P56719 rattus norv
7	1319.5	68.1	444	1	OX2R_CANFA	Q9tup7 canis famil
8	1315.5	67.9	443	2	Q6VLX3	Q6vlx3 mus musculu
9	1315.5	67.9	443	2	AAR01327	Aar01327 mus muscu
10	1315.5	67.9	443	2	AAR11294	Aar11294 mus muscu
11	1315.5	67.9	460	1	OX2R_MOUSE	P58308 mus musculu
12	1315.5	67.9	460	2	AAR01328	Aar01328 mus muscu
13	1315.5	67.9	460	2	AAR11293	Aar11293 mus muscu
14	1313.5	67.8	444	1	OX2R_HUMAN	O43614 homo sapien
15	1313.5	67.8	444	2	AAG28021	Aag28021 homo sapi

16	1257	64.9	364	2	Q8BV78	Q8bv78 mus musculu
17	1099	56.7	260	1	OX1R_MOUSE	P58307 mus musculu
18	945	48.8	199	2	Q80T45	Q80t45 mus musculu
19	654.5	33.8	166	2	Q8MJ13	Q8mj13 ovis aries
20	591	30.5	127	2	Q8SPR4	Q8spr4 ovis aries
21	510	26.3	109	2	Q8I010	Q8i010 bos taurus
22	483.5	25.0	430	1	NFF1_HUMAN	Q9gzq6 homo sapien
23	480.5	24.8	432	1	NFF1_RAT	Q9ep86 rattus norv
24	480	24.8	417	1	NFF2_MOUSE	Q924h0 mus musculu
25	476.5	24.6	405	2	Q924N0	Q924n0 mus musculu
26	473.5	24.4	522	1	NFF2_HUMAN	Q9y5x5 homo sapien
27	467.5	24.1	417	1	NFF2_RAT	Q9eqd2 rattus norv
28	457	23.6	399	2	Q75XU5	Q75xu5 gallus gall
29	457	23.6	399	2	BAC87782	Bac87782 gallus ga
30	453	23.4	432	2	Q924G9	Q924g9 rattus norv
31	444.5	22.9	758	2	Q7YU49	Q7yu49 drosophila
32	427.5	22.1	464	2	Q9VB87	Q9vb87 drosophila
33	427.5	22.1	464	2	AAF56655	Aaf56655 drosophil
34	422.5	21.8	449	1	NYR_DROME	P25931 drosophila
35	422	21.8	353	2	Q7PRC5	Q7prc5 anopheles g
36	415	21.4	370	2	Q6VMN6	Q6vmn6 mus musculu
37	415	21.4	370	2	AAQ84215	Aaq84215 mus muscu
38	412.5	21.3	375	2	O57463	O57463 brachydanio
39	411.5	21.2	370	1	GP10_RAT	Q64121 rattus norv
40	411	21.2	370	1	GP10_HUMAN	P49683 homo sapien
41	409	21.1	86	1	OX1R_PIG	O97661 sus scrofa
42	406	21.0	517	2	Q9VWR3	Q9vwr3 drosophila
43	406	21.0	598	2	Q9VWQ9	Q9vwq9 drosophila
44	403.5	20.8	542	2	Q9VRM0	Q9vrm0 drosophila
45	403.5	20.8	542	2	AAF50775	Aaf50775 drosophil

ALIGNMENTS

RESULT 1

OX1R_HUMAN

ID OX1R_HUMAN STANDARD; PRT; 425 AA.

AC O43613;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Oxlr) (Hypocretin receptor type 1).

GN Name=HCRTR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,

RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,

RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,

RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,

RA Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides

RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
 CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
 CC exclusively coupled to the G(q) subclass of heteromeric G
 CC proteins, which activates the phospholipase C mediated signaling
 CC cascade (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF041243; AAC39601.1; -.
 DR Genew; HGNC:4848; HCRTR1.
 DR MIM; 602392; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 46 Extracellular (Potential).
 FT TRANSMEM 47 67 1 (Potential).
 FT DOMAIN 68 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 102 2 (Potential).
 FT DOMAIN 103 119 Extracellular (Potential).
 FT TRANSMEM 120 142 3 (Potential).
 FT DOMAIN 143 164 Cytoplasmic (Potential).
 FT TRANSMEM 165 185 4 (Potential).
 FT DOMAIN 186 216 Extracellular (Potential).

FT TRANSMEM 217 239 5 (Potential).
 FT DOMAIN 240 298 Cytoplasmic (Potential).
 FT TRANSMEM 299 321 6 (Potential).
 FT DOMAIN 322 336 Extracellular (Potential).
 FT TRANSMEM 337 360 7 (Potential).
 FT DOMAIN 361 425 Cytoplasmic (Potential).
 FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 425 AA; 47521 MW; 1634083DE10CA092 CRC64;

Query Match 96.8%; Score 1875; DB 1; Length 425;
 Best Local Similarity 98.6%; Pred. No. 1.5e-120;
 Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
 |||||
 Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCK 120
 |||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFGHALCK 120
 Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSSILGIWAVSLAIMVPQA 180
 |||||
 Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLEFKSTARRARGSSILGIWAVSLAIMVPQA 180
 Qy 181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||: |||||
 Db 181 AVMECSSSVLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||
 Db 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 2

Q9HBV6

ID Q9HBV6 PRELIMINARY; PRT; 425 AA.

AC Q9HBV6

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypocretin receptor-1 (Orexin receptor 1).

GN Name=HCRTR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;
 RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
 RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
 RA Pedrazzoli M., Padigar M., Kucherlapati M., Fan J., Maki R.,
 RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
 RT "A mutation in a case of early onset narcolepsy and a generalized
 RT absence of hypocretin peptides in human narcoleptic brains.";
 RL Nat. Med. 6:991-997(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21580342; PubMed=11723285;
 RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
 RA Stefansson K., Gulcher J.R.;
 RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
 RL Neurology 57:1896-1899(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Olafsdottir B.R., Stefansson R.H., Sigurdsson A., Hannesson H.H.,
 RA Sainz J., Scammell T.E., Stefansson K., Gulcher J.R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yeager M., Welch R., Haque K., Bergen A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF202084; AAG28020.1; -.
 DR EMBL; AF202078; AAG28020.1; JOINED.
 DR EMBL; AF202079; AAG28020.1; JOINED.
 DR EMBL; AF202081; AAG28020.1; JOINED.

DR EMBL; AF202083; AAG28020.1; JOINED.
 DR EMBL; AF202082; AAG28020.1; JOINED.
 DR EMBL; AF202080; AAG28020.1; JOINED.
 DR EMBL; AY062030; AAL47214.1; -.
 DR EMBL; AY070269; AAL50221.1; -.
 DR EMBL; BC074796; AAH74796.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016499; F:orexin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 96.5%; Score 1869; DB 2; Length 425;
 Best Local Similarity 98.3%; Pred. No. 3.9e-120;
 Matches 357; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSAVLTLFSFIPLDRWYAICHPLLEFKSTARRAGSILGIWAVSLAIMVPPQA	180
Db	121	VIPYLQAVSVSAVLTLFSFIPLDRWYAICHPLLEFKSTARRAGSILGIWAVSLAIMVPPQA	180
Qy	181	AVMQSSSVLPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
		:	
Db	181	AVMECSSVLPELANRTRFLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 3

OX1R_RAT
ID OX1R_RAT STANDARD; PRT; 416 AA.
AC P56718;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).
GN Name=Hcrtrl;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98150861; PubMed=9491897;
RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
CC exclusively coupled to the G(q) subclass of heteromeric G
CC proteins, which activates the phospholipase C mediated signaling
CC cascade.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in the brain in the
CC prefrontal cortex, hippocampus, paraventricular thalamus,
CC ventromedial hypothalamus, arcuate nucleus, dorsal raphe nucleus,
CC and locus coeruleus. Not detected in the spleen, lung, liver,
CC skeletal muscle, kidney and testis. Orexin receptor mRNA
CC expression has also been reported in the adrenal gland, enteric
CC nervous system, and pancreas.
CC -!- INDUCTION: By nutritional state, up-regulated by fasting.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 4

Q6VNS3

ID Q6VNS3 PRELIMINARY; PRT; 416 AA.
 AC Q6VNS3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeve H.S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336083; AAR01326.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 416 AA; 46766 MW; A8958C594C365E00 CRC64;

Query Match 90.5%; Score 1753; DB 2; Length 416;
 Best Local Similarity 92.6%; Pred. No. 3.4e-112;
 Matches 336; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60
 ||| :|||
 Db 1 MEPSATPGAQPGVPTSSGEPFHLPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFLIA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 |||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
 ||| :|||
 Db 121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAVMVPQA 180

Qy 181 AVMQSSSVLPPELANRTRFLSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

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      |||: |||||:| |||:||||| |||||
Db      181 AVMECSSVLPELANRTRLFVSCDEHWADELYPKIYHSCFFIVTYLAPLGLMGMAFYQIFR 240
Qy      241 KLWGRQIPGTTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||||:| ||| ||||| |||||
Db      241 KLWGRQIPGTTTSALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300
Qy      301 MVVLLVFALCYLPISVLNVLKRVEFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||||:| ||| ||||| |||||
Db      301 MVVLLVFALCYLPISVLNVLKRVEFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
      |||
Db      361 LSG 363

```

RESULT 5

AAR01326

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ID   AAR01326      PRELIMINARY;          PRT;   416 AA.
AC   AAR01326;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Orexin receptor type-1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c;
RA   Chen J., Rande H.S.;
RT   "Cloning and Characterization of the Mouse Type-1 Orexin Receptor
RT   (OX1R).";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY336083; AAR01326.1; -.
KW   Receptor.
SQ   SEQUENCE   416 AA;  46766 MW;  A8958C594C365E00 CRC64;

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Query Match      90.5%;  Score 1753;  DB 2;  Length 416;
Best Local Similarity  92.6%;  Pred. No. 3.4e-112;
Matches 336;  Conservative  8;  Mismatches  19;  Indels  0;  Gaps  0;

```

```

Qy      1 MEPSATPGAQMGPVPPGSPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
      ||||| ||| | || :||||| ||||| ||||| ||||| ||||| |||||
Db      1 MEPSATPGAQPGVPTSSGEPFHLPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFLIA 60
Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQALCK 120
Qy      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSVILGIWAVSLAIMVPQA 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARGSVILGIWAVSLAVMVPQA 180
Qy      181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||: |||||:| |||:||||| ||||| |||||

```

Db 181 AVMECSSVLPELANRTRLFSVCDEHWADELYPKIYHSCFFIVTYLAPLGLMGMAFYQIFR 240
 QY 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||:| | | | |
 Db 241 KLWGRQIPGTTTSALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300
 QY 301 MVLLLVFALCYLPISVLNVLKRVFQGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||
 Db 301 MVLLLVFALCYLPISVLNVLKRVFQGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 QY 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 6

OX2R_RAT

ID OX2R_RAT STANDARD; PRT; 460 AA.
 AC P56719;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=Hcrtr2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98150861; PubMed=9491897;
 RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
 RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
 RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
 RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
 RA Yanagisawa M.;
 RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
 RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998).
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in the brain in the cerebral cortex,

Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYQLQAVSVSVAVL	135
		: : : :	
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLTVSVSVSVL	143
Qy	136	TLSFIPLDRWYAICHPLLEFKSTARRARGSILGIWAVSLAIMVPAQAVMQSSSVLPPELANR	195
		: : : : : : :	
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIWMERSSMLPGLANK	203
Qy	196	TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRWLWGRQIPGTTALV	255
		: : : : : : :	
Db	204	TTLFTVCDERWGGEVYPKMYHICFFLVTYMAPLCLMVLAYLQIFRWLWCRQIPGTSSVVQ	263
Qy	256	RNWKRPDQLGDLQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV	306
		: : : : :	
Db	264	RKWKQP-----QPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV	312
Qy	307	FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG	363
		: :	
Db	313	FAICYLPISILNVLKRVFGMETHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSG	369

OX2R CANFA

ID OX2R CANFA STANDARD; PRT; 444 AA.

AC 09TUP7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).

GN Name=HCRTR2;

OS *Canis familiaris* (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99385793; PubMed=10458611;

RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,

RA de Jong P.J., Nishino S., Mignot E.;

RT "The sleep disorder canine narcolepsy is caused by a mutation in the

RT hypocretin receptor 2 gene.";

RL Cell 98:365-376 (1999).

RN [2]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408 (2001).

RN [3]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and

RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458 (2001).

RN [4]

RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.
 RX MEDLINE=21180003; PubMed=11282968; DOI=10.1101/gr.161001;
 RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;
 RT "Identification and functional analysis of mutations in the hypocretin
 RT (orexin) genes of narcoleptic canines.";
 RL Genome Res. 11:531-539(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Defects in HCRTR2 are a cause of an autosomal recessive
 CC form of narcolepsy, observed in labradors, dobermans and
 CC dachshunds. Narcolepsy is a neurological sleep disorder affecting
 CC animals and humans, characterized by excessive daytime sleepiness,
 CC sleep fragmentation, symptoms of abnormal rapid-eye-movement
 CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and
 CC sleep paralysis. Cataplexy is a sudden loss of muscle tone
 CC triggered by emotions, which is the most valuable clinical feature
 CC used to diagnose narcolepsy. As in humans, most cases of canine
 CC narcolepsy are sporadic but an autosomal recessive form was also
 CC observed.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF164626; AAD49333.1; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Disease mutation; G-protein coupled receptor; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).

FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 54 54 E -> K (in autosomal recessive
 FT narcolepsy).
 FT MUTAGEN 54 54 E->K: Loss of function.
 SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;

Query Match 68.1%; Score 1319.5; DB 1; Length 444;
 Best Local Similarity 71.4%; Pred. No. 1.8e-82;
 Matches 250; Conservative 42; Mismatches 51; Indels 7; Gaps 3;

Qy 17 SREPSVPDPDYED-EFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
 ::|| | ||:| |||||:|:|:| ||||| | : ||||| |||:|:|
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALVGNVLCVAVWKNH 83
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHGHALCKVIPYLQAVSVSVAVL 135
 |||||:|:|:| |||||:| || :||| ||||| ||||:|
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143
 Qy 136 TLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQAAMQSSSVLPELANR 195
 ||| | |||||:|:|:| ||: || || ||:| ||: |:| |||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVIIWVSCIIMIPQAIVMECSTMLPGLANK 203
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
 | ||:| ||| :||:| |||:|:| || :| ||||| ||||:| :
 Db 204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCMLVLAYLQIFRKLWCRQIPGTSSVVQ 263
 Qy 256 RNWK--RPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLLVFALCYLP 313
 | || :| :| :| :| ||:|:| |||||:| |||||:| |||
 Db 264 RKWKPLQPASQ---PRGPGQQTksrisavaaeikqirarrktarmlmvlllvfaicylp 319
 Qy 314 ISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:| ||||| ||| ||| ||||| ||||| ||||| |||||
 Db 320 ISILNVLKRVFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 8

Q6VLX3

ID Q6VLX3 PRELIMINARY; PRT; 443 AA.
 AC Q6VLX3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 GN Name=MOXR2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Rande H.S.;
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeve H.S.;
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
 RT gene.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11294.1; JOINED.
 DR EMBL; AY339384; AAR11294.1; JOINED.
 DR EMBL; AY339385; AAR11294.1; JOINED.
 DR EMBL; AY339386; AAR11294.1; JOINED.
 DR EMBL; AY339387; AAR11294.1; JOINED.
 DR EMBL; AY339388; AAR11294.1; JOINED.
 DR EMBL; AY339389; AAR11294.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 67.9%; Score 1315.5; DB 2; Length 443;
 Best Local Similarity 70.3%; Pred. No. 3.3e-82;
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy 17 SREPSVPDPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
 :|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:|:|
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYQLQAVSVSVAVL 135
 ||||| ||||| |||||:|:|:| | | : ||||| || ||||:|
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLQTVSVSVSVL 143
 Qy 136 TLSFIPLDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMV PQA AVMQSSSVLP ELANR 195
 || | ||||| |||||:|:|:| ||: | | ||:| | | : ||:| |||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVVIWIVSCIIMIPQAIVMEC SMLPGLANK 203
 Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
 | ||:| | | :||:| |||:|:| || | :| ||||| |||||:| :
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263
 Qy 256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
 | ||: :| :| |||| | ||:|:| |||||:| |||||
 Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:| |||||:| ||||| || || || ||||| ||||| |||||
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 11

OX2R_MOUSE

ID OX2R_MOUSE STANDARD; PRT; 460 AA.
 AC P58308; Q8BG12;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=Hcrtr2; Synonyms=Mox2r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteu G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE OF 100-311 FROM N.A.
 RC STRAIN=C57BL/6;
 RA Szendro P.I., Maevers K., Eichele G.;
 RT "Cloning of mouse orexin receptors."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy."
 RL Bioessays 23:397-408(2001).
 RN [4]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness."

RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL; AK038551; BAC30039.1; -.
 DR EMBL; AK048781; BAC33457.1; -.
 DR EMBL; AF394597; AAK71327.1; -.
 DR MGD; MGI:1889024; Mox2r.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 460 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 201 201 A -> T (in Ref. 2).
 FT CONFLICT 240 240 I -> V (in Ref. 2).
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 67.9%; Score 1315.5; DB 1; Length 460;
 Best Local Similarity 70.3%; Pred. No. 3.4e-82;
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

QY 17 SREPSVPPDYED-EFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVALVGNLTLCVAVWRNH 75
 :|| | ||:| |||||:|:|:| ||||| | : |||||:| |||:|:|:
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy 136 TLSFIPLDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVMQSSSVLPELANR 195
 ||| | ||||| ||||| : ||||| : || || || : ||| || : ||| ||| :
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSMLPGLANK 203

Qy 196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
 | ||:| | | :|||:| | ||:| | :| | ||||| |||||:| :
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263

Qy 256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVVLLV 306
 | ||: :| :| ||| | ||:| | ||||| : |||||
 Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVVLLV 312

Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||:|||||:||||||| ||| ||| ||||| ||||| |||||
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 13

AAR11293

ID AAR11293 PRELIMINARY; PRT; 460 AA.
 AC AAR11293;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2b.
 GN MOXR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeve H.S.;
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
 RT gene.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11293.1; JOINED.
 DR EMBL; AY339384; AAR11293.1; JOINED.
 DR EMBL; AY339385; AAR11293.1; JOINED.
 DR EMBL; AY339386; AAR11293.1; JOINED.
 DR EMBL; AY339387; AAR11293.1; JOINED.
 DR EMBL; AY339388; AAR11293.1; JOINED.
 DR EMBL; AY339389; AAR11293.1; JOINED.
 DR EMBL; AY339390; AAR11293.1; -.
 KW Receptor.
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 67.9%; Score 1315.5; DB 2; Length 460;
 Best Local Similarity 70.3%; Pred. No. 3.4e-82;
 Matches 251; Conservative 40; Mismatches 45; Indels 21; Gaps 4;

Qy 17 SREPSVPDPDYED-EFLRYLWRDYLYPEYEWVLIAYVAVFVVALVGNTLVCLAVWRNH 75
 ::|| | ||:| ||||| :||:| ||||| | : |||||:| |||:| |||
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135

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      |||:|:||||:| || :||||||| ||||:|
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLOTVSVSVSVL 143

Qy      136 TLSFIPLDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQAAMQSSSVLPELANR 195
      ||| | |||:||||:||||:| ||: || || ||:| || ||: ||:| |||:
Db      144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSLMLPGLANK 203

Qy      196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTTALV 255
      | ||:| | | :||:| |||:||||:| || :| ||||| ||||:| :
Db      204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263

Qy      256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
      | ||: :| :| |||| | ||:||||:||||:|
Db      264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312

Qy      307 FALCYLPISVLNVLKRIVFGMFQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
      ||:|||||:||||||| ||| ||| |||:||||:||||:|
Db      313 FAICYLPISILNVLKRIVFGMFTHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSG 369

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RESULT 14

OX2R_HUMAN

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ID   OX2R_HUMAN      STANDARD;          PRT;   444 AA.
AC   O43614;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
GN   Name=HCRTR2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98150861; PubMed=9491897;
RA   Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA   Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA   Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA   McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA   Yanagisawa M.;
RT   "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT   and G protein-coupled receptors that regulate feeding behavior.";
RL   Cell 92:573-585(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21580342; PubMed=11723285;
RA   Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA   Stefansson K., Gulcher J.R.;
RT   "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL   Neurology 57:1896-1899(2001).
RN   [3]
RP   REVIEW.
RX   MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA   Hungs M., Mignot E.;
RT   "Hypocretin/orexin, sleep and narcolepsy.";
RL   Bioessays 23:397-408(2001).

```

RN [4]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041245; AAC39602.1; -.
 DR EMBL; AY062031; AAL47215.1; -.
 DR Genew; HGNC:4849; HCRTR2.
 DR MIM; 602393; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).

SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 67.8%; Score 1313.5; DB 1; Length 444;
Best Local Similarity 70.0%; Pred. No. 4.6e-82;
Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

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Qy      17 SREPSPVPPDYED-EFLRYLWRDYLKPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
          ::|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:| |
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCKVIPYLQAVSVSVAVL 135
          |||||:|:|:| |||||:|:|:| || : ||||| ||||:| |
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIPLDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQAAMQSSSVLPELANR 195
          ||| | |||||:|:|:| || | : || | ||:| || | : | | ||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTVFPLANK 203

Qy     196 TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
          | ||::| ||| :||:| |||:|:| || | :| | ||||| ||||:| :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFIVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
          | || | ||| | ||:|:| |||||:| |||||
Db     264 RKWK-----PLQPVSQPRGPGQPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312

Qy     307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
          ||:| ||||:| ||||| || || ||||| ||||| |||||
Db     313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369
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RESULT 15

AAG28021

ID AAG28021 PRELIMINARY; PRT; 444 AA.

AC AAG28021;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypocretin receptor-2.

GN HCRTR2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;

RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,

RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,

RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,

RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;

RT "A mutation in a case of early onset narcolepsy and a generalized

RT absence of hypocretin peptides in human narcoleptic brains.";

RL Nat. Med. 6:991-997(2000).

DR EMBL; AF202091; AAG28021.1; -.

DR EMBL; AF202085; AAG28021.1; JOINED.

DR EMBL; AF202086; AAG28021.1; JOINED.

DR EMBL; AF202087; AAG28021.1; JOINED.
DR EMBL; AF202088; AAG28021.1; JOINED.
DR EMBL; AF202089; AAG28021.1; JOINED.
DR EMBL; AF202090; AAG28021.1; JOINED.
KW Receptor.
SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 67.8%; Score 1313.5; DB 2; Length 444;
Best Local Similarity 70.0%; Pred. No. 4.6e-82;
Matches 250; Conservative 37; Mismatches 49; Indels 21; Gaps 3;

Qy	17	SREPSVPVPPDYED-EFLRLYLWRDYLYPEKQYEWVLIAAYVAVFVALVGNTLVCLAVWRNH	75
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Db	24	TQEPFLNPSTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRVTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYQLQAVSVSVAVL	135
		: : : : :	
Db	84	HMRVTVTNYFIVNLSLADVLVTITCLPATLVDDITETWFFGQSCLKVIPYQLQTVSVSVSVL	143
Qy	136	TLSFIPLDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQAAMQSSSVLPPELANR	195
		: : : : : : :	
Db	144	TLSCIALDRWYAICHPLMEFKSTAKRARNSIVIWIWVSCIIMIPQAIVMECSTVFPGLANK	203
Qy	196	TRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRWGRQIPGTTSALV	255
		: :: : : : : : :	
Db	204	TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCMLVLAYLQIFRWLRQIPGTSSVVQ	263
Qy	256	RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVVLLV	306
		: : :	
Db	264	RKWK-----PLQPVSQPRGPQGPTKSRRMSAVA AEIKQIRARRKTARMLMVVLLV	312
Qy	307	FALCYLPISVNLVLRVFGMFVRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG	363
		: :	
Db	313	FAICYLPISILNVLRVFGMFAHTEDRETVEAWFTFSHWLVYANSAANPIIYNFLSG	369

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Job time : 98.8388 secs